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Sequence 1 Sequence 3

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US-08-319-387-1
Sequence 1, Application US/08319387
Sequence I. Application US/08319387
Setent No. 543317
Setent No. 543317
APPLICANT: Shalds, Malcolm S. APPLICANT: Francesconi, Stephen C. TITLE OF INVENTION: Microbial Degradation of Trichloroethylene, TITLE OF INVENTION: Dichloroethylenes and Aromatic Pollutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,387
US-09-120-249-3

US-08-804-227C-1

US-08-804-227C-1

US-08-295-060-3

US-08-875-034A-1

US-08-875-034A-1

US-08-872-283-1

US-08-482-385A-1

US-08-482-385-4

US-08-482-199-2

US-08-528-199-5

US-08-528-199-5
                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US95-04801-1
US-08-533-669A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/167,457
FILING DATE: 15-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/694,718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 02-MAY-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/POCKET NUMBER: UMF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: DNA (genomic) US-08-319-387-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9785 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LECURATIONS: 904-5,2
TELEPHONE: 904-372-5800
1227
43280
13987
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666
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STRANDEDNESS: single
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
  USA
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                                                                                                                                                                                                                                                                                                                                    1 gatcatttcatcaaatgcgc.....tcggcccgggcaacacgatc 5828
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/5C_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/6_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-804-198-1
US-08-576-626A-1
US-08-440-856A-9
US-08-924-847A-1
US-08-120-052-1
US-09-120-052-1
US-08-125-1
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                                                                                                                                                                              September 26, 2000, 15:48:05
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                              sw model
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                                                                                                                              - nucleic search, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq length: 0 seq length: 2000000000
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5828
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Match Length
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Sequence

772.4 772.7 772.7 660.6 600.6 600.6 590.7 590.7 590.7 590.7 590.7 590.7 590.7 590.7 590.7 590.7

Score

Result

58.8 58.4 58.4

ch 1 Similarity 70.3%; Score 2490.6; DB 1; Length 9785; 518; Conservative 0; Mismaţches 1369; Indels 156; Gaps 15;	aggagcaagaagtgaccatcgagctgaagacaftcgacatcaagccgctccggcacacct 511 	lgogcatgtcgcgcagaacatcggcggcgacgacggcgacgcgctaccaggaaggca 571 	gatgggcgcagcccaggagaacttccattaccggccgacctgggacccggactacg 631 	agatcttcgatccgtcgcgctcggcgatccggatggcgaactggtacgcgttgaaggatc 691 	gegecagttctactacgegtcgtggggacacgggggggggcaagaggatgcgatgg 751 	agtcgaacttcgagttcgtcgaatcgcgccggatgatcggcctgatgcgcgacgacgtgg 811 	rgcgcgggcgctcgacgtgctgccgctdccgccgcgcgtggggcgcgaacatga 871 	acaacgcgcagatctgcgcgctcggctacggcacggtgttcaccgcgcccgcgatgttcc 931 	atgcgatggacaactcggcgtcgcgcaatacctcacgcgtctcgcgctcgcgatggccg 991 	agcccgacgtgctggaggcgaccaaggcgacctcgcgacgcctggcagccgc 1051 	gegecgetaegtegagaeacgetggtegtegecgateeggtegagetgtteategege 1111 	agaacttggcgctcgacggctgtatccgctcgtctacgaccgcttcgtcgacgaac 1171 	natogostcgaaggosgstcggcagtcgcgatgctgaccgcgttcatgcccgaatggc 1231	raccgagtcgaaccgctggatcgacgcggtcgtgaagacgatggccgccgaatccgacg 1291 	acaaccgcgctgctcgcccgctggacadgcctggtccgcgcgcgcgcggcggcac 1351 	ggcaccggtggcggcgctgcaggatgccgggcgcgcgctcgacgaagtgc 1411 	gcgagcagttccacgcacgcggccaggtcggcatcgcgctctgacgacgggaatcct 1471 1111
Query Match Best Local S Matches 3618	452 agga 2861 AGG	512 ttgc 2921 ACAC	572 tgat 2981 CTG1	632 agat 3041 AACT	692 cgcg 3101 CGCG	752 agtc 3161 AATC	812 ccgc 3221 GACA	872 acae 3281 ACAA	932 atgo 1 3341 ACGO	992 agcc 3401 GACC	1052 tgcg 3461 TGCG	1112 agaa 3521 AAA	1172 ggato 3581 ACATO	1232 acac 3641 ATGA	1292 acaa 3701 ATAA	1352 tggc 3761 TGTT	1412 gcga
Oue Bes Mat	Qy	Qy Dp	QY Db	Oy Dp	oy Db	Qy	Qy	Qy Db	Qy Db	Qy Db	O.y D.b	Qý Dp	O.Y Db	O.y DD	Oy Dp	Oy Dp	Oy Dp

3999 4119 4223 1948 4343 4403 4463 2128 4523 2188 2248 4643 2308 2368 2428 4823 2548 4943 ---gcatgtccaacgtattcatcgcctttcaggccaatg 3880 TICCIGACCGICATAGAGGAATGTICATGTCTAACGTATITATCGCGTTTCAGGCTAACG agtcgcccggcatggtcaagatcgacgcggaccggctgacgatccgccgcgaaacga cgcgccacgcgcaccgacacaccggagacacgaatggacacgccaacgctcaagaaaaa GCC-------AAAGAGGAAATTGAAATGGACACTTCTGTGCAGAAGAAGAA AATCGCCTGGCATGGTGAAGATCGATGCGCCCGGGCATCTCACAATAAACCGTCAAAAGCA ccagocgatggacaaggtottcccgtacgaccgctacgagggcatcaagatccacgactg ccgcgtgtggtacctgtcggtgccgaagtcgttcttcgagggacgcgtattcgtcgggggcc GGAGTATATGGCACACCGAGGTTTTGCCCACATTGGTCGGCATTTTACGGGTGAAGGGGC cccttaacccaaggaatgcca 3940 4000 1649 4060 4120 1769 4180 4584 4884 1472 1529 1589 1709 1829 4224 1889 4284 1949 4344 2009 4404 2069 4464 2129 4524 2189 2249 4644 2309 2369 4704 4764 2429 4824 2489 g q Q Óγ δ Ω g δ ò g οy g õ qq δ g ò g ŏ g ò q ò Dp g ò QQ g q δ ò ŏ δ 유

2549	ctcaaacaggacccagacaacgfaccgatcatacagcaatcaaatca
4	00
09	gegeggetaceggetgetgaegetggtegegatgatgaegaetacatgeageceaageg 2668
669 064	cgtgatgagctggcgagtcgtgggagtgtacgccgagcagaacggcgcgctgtt 2728
729	78
	ouaiciicciialGocaiccocaagcocccaagggciGgGaCcaggGTTGCGAAG ggatcacatcagccaccaggggtggtcgacgttctacggcttcaacgggcctcgg
80	3ccc 523
	ttccacacctgggtgccgaccgaagacgaaatgggctggct
240	ccacaccressricccacaaasaaarsdaarissscrigiccsagaaagaccccga 529
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969 360	caaccgcttctacatgaagacgctgccgatgctgtgccagacgtgccagatcccgatgct 3028
029	10909090000000000000000000000000000000
089	agttccacttctgcagcgaccactgcaagacatcttcgatcacgagccgcagaata 314
4	gtgcaggcgtgccggtgccacagatccagggcaactcgcgccggtgc 320
540	
209	ggaccegggegeggaggettegatecgetegeeggggegetegaetaetaegeggtgae 3268
269	gatgggccgcgacaacctcgatttcgacggctcggaagaccagaagaacttcgcggcgtg 3328
29	egeggecaggegeaactgaccegeaacgacaageaatettgacgaggecegeg 338
720	
389	44
າ .	-ANGGAGGAGGAGGAGGGTIGTIGTIGCCCTCAAA 3//
449	ccctacgacttcccggtgaaggatgccgtcgagaagtttccggcgccgctgctctacgtg 3508
509	ctgccgcccgaca
831	CTGGGAAGACCATCTGTTGTTTGCGGCACCTGTTGCCTTGCCCTGCCG
	gttcggcgcgtggccggcgacqtgctgccgtctacggctatcaccccgacttc 362
	TTCGGTGCGCTGTGCACCCAGGTGTTGCCCGGCACTTATGGCTATCACCCCGATTTC 59
29	gcgaagatcgactgggatcgcgtcgagtggttccggtcgggcgagccgtgggcgccggac 3688

3995 6989 4055 6010 3808 6130 3815 6249 6309 4115 6487 4175 6427 6547 2099 4475 6727 6907 cccggcctcgacggcctcggcggcgagcttctgaccgccacgcggacgagcgaaccat CCTGGCTTGAACGGTCTGAGCGGTTCCTGCAATTGAGATTGCGTCATGGCAGCGCAATCA ggcacctgcaaggtcgccgtgctcgacggcgagaccgatcccggcgatgcgaacccgttc atgago CACCGCAGCCGAAGTTACAGGCCGCGGTGTGGATTTGGCCTCCGGCGATTTGAACAATGACC ctcgatgccgcgctgcgccagggcatctacattccgcacgcgtgctgtcacgggctgtgc gcgctgatggatttcgagcgcgaggaaggcaaggcgctcgcgtgctgcgacgctgcag cgcctgaagctgtcgcagccgatccgcttccaggcgggccagtacgtgcagctcgagatt 6548 TICCIGAGACICGAICAACCGAITCAITIICAGGCGGGICAGIACGIGCAACTIGAAAII tacggtcagcgcagcgcaggagctctactaccacgacgaattccgcgcgctggccgaa -----6191 8099 6131 6250 3936 6310 6428 6488 8999 5951 3689 6011 3749 6071 3809 3816 3876 3666 6370 4056 4116 4176 4236 4296 6728 4416 4356 6788 4476 6848 4536 8069 4596 4656 2969 a οy qq Qy Db οy QQ Q B S S S δ q δy QQ οy g δ QQ q Op q q g ò ŏ ŏ οy õ δ g ò a QQ δ δ

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3909 GTGCAAGCACGGGGCTGCGGACCTGCAAGGTCCGGCTGCTCGACGGGGGACGTAGAGGA 3968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
STRAIN: No. 5612204ardia corallina B-276 (FERM P-4094; FERM
STRAIN: BP-5124; ATCC 31338)
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Pred. No. 7.4e-31;
0; Mismatches 410; Indels
                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: & WordPerfect version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP Hei-6-179689
FILING DATE: 08-JUL-1994
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 3805..4830
; OTHER INFORMATION: /product= "amoD" US-08-499-215-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLGGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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illarity 54.9%;
Conservative (
                                                                ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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   D.C.
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LOCATION: 910..1935
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CLASSIFICATION: 435
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   Washington
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Best Local Similarity
Matches 546; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION
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                                                                4716 gggcaccaggcgtacctgtgcgggccgccgcgatgatcgacgcgtgcatcacgacgctg
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                                                                                                                                        7087 GGCCACAAAGCCTATTTGTGCGGGCCGCCGGCAATGATCGACGCCTGCGTCACGACCCTG
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APPLICANT: Saeki, Akira
APPLICANT: Miura, Akira
TITLE OF INVENTION: BIOLOGICAL DEGR.
TITLE OF INVENTION: TREATMENT OF CH.
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, M.
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Patent No. 5612204
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                                                                                        4266 CTCGCTGGCAAACGCCCCTGACGA------CCCGTCAGTGGTGGAGCTGATCTGCAA 4316
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                                                                                                                                                           4317 GCTCTACCCGGATGGCCTCTTCTCCCGCTTCTGAGGGACGAGGCTGCCCCGGGCACGCC 4376
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Patent No. 5543317
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32606
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5524 tgctgcccgaaggcgcgctgccggcggtcggccgccaactgcggttcctgctgccgagcg 5583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACATGAGATGCGTCTGTTTGCGACGAAGGAATATGTGGGCCACCGGAGTCGGAACGACCA
                                                                                                                                                                                                                                                                                                                                                                                                         Length 9785;
                                                                                                                                                                                                                                                                                                                                                                                                       Score 137.2; DB 1;
Pred. No. 2e-18;
0; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: DeHOff, Bradley S.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Stuton, Kimberly L.
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                 US 07/694,718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08804227C Patent No. 5876991
GENERAL INFORMATION:
                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/POOKET NUMBER: UWF-7
TELECOMMUNICATION INFORMATION:
TELEFAX: 904-375-8100
TELEFAX: 904-375-8100
TELEFAX: 904-375-8100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9785 base pairs
                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                         2.48;
70.18;
                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 02-MAY-1991
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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FILING DATE: 15-DEC
CLASSIFICATION: 435
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Best Local Similarity
Matches 213; Conservat
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29286 GGTCCCCGCGGTGTTCCTCACGCCCTACGTCACCCTGGCCCTCAGGCC 29345
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                                1467 atcctcccttaacccaaggaatgccagcatgtccaacgtattcatcgcctttcaggccaa 1526
                                                                                                                                                                                                1587 cgagtcgcccggcatggtcaagatcgacgcgccggaccggctgacgatccgccgcgaaac 1646
                                                                                                                                                                                                                                                                                  1647 gatcgaggaactgaccggcacgcgttcgacctgcagcagctccaggtcaacctgatcac 1706
                                                                                                                                                                                                                                       29226 GGCCGACCACCGCTGCTCGCCCCGGTCCTGGTCCTACGCCCAGGCCGCCTC
                                                                                                                  GENERAL INFORMATION:
APPLICANT: Burgett, Stanley G.
APPLICANT: Knustoss, Stuart A.
APPLICANT: Rao, Nagaraja R.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Rosteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                        29346 GGGGGAGCGGTGCTCGTGCACGCCGCCGGG 29379
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MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,198
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STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08804198 Patent No. 5945320
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ATORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 35,470
REFERENCE/DOCKET NUMBER: P911
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACIERISTICS:
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TYPE: nucleic acid
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COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: PEDVUARY 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
RAGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION ON 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 44377 Dasse pairs
TYPE: INCORMATION:
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US-08-804-227C-7
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                                                                                                                                             1.2%; Score ... 1e-U2, 43.5%; Pred. No. 1e-U2, ... 0; Mismatches 426; ...
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Patent No. 5998194
GENERAL INFORMATION:
APPLICANT: Summers, R.G.
APPLICANT: Ratz, L.
APPLICANT: Donadio, S.
CDS
31329..36071
                                                         CDS
36155..41830
                                                                                                                                                                                             Matches 328; Conservative
                                                                                                                                                                       Local Similarity
NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
                                                                           ; LOCATION:
US-08-804-198-1
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US-08-576-626A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGCGACGGTGCACCCACGCGGACCTGGCACCCCCGCGCGATCCACGCGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     toggogtogogaatacctcacgcgtctcgcgctcgcgatggccgagcccgacgtgctgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1976 ACGICGACGCCGAGAICAICGCGACCTICGACGCGCAGCAGCAGAAGGCGTCGCGAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1067 aggacacgetggtcgtcgccgatccggtcgagctgttcatcgcgcagaacctcgcgctcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCCGCACAACGTCCGCACGGTCGGCTTCGTCCCGATGCACGCGCTGCTGCCGACCTGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 72.2; DB 4;
Pred. No. 7.4e-06;
0; Mismatches 308;
APPLICANT: Staver, M.J.
TITLE OF INVENTION: POLYKETIDE-ASSOCIATED SUGAR
TITLE OF INVENTION: BIOSYNTHESIS GENES
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FESTEED VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/576,626A
FILING DATE: 21-DEC-1995
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5857.US.01
                                                                                                                                  3: Abbott Laboratories
100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-40,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 938-3137
TELEFAX: (847) 938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.2%;
Best Local Similarity 47.4%;
Matches 283; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENY INFORMATION:
NAME: Dianne Casuto
REGISTRATION NUMBER: P-4(
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 3756 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                               ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                       CITY: Abbott Park
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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NAME/KEY: misc_feature
LOCATION: 4471..5847
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACFsynhase domain of module"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: 7165..9216
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: dehydratase and enoylreductase domains m"
                                                                                                                                                                                                                                                                                                                                  NAME/KEX: misc_feature
LOCATION: 3406..3921
OTHER INFORMATION: Chuction= "approximate span of OTHER INFORMATION: beta-ketoreductase domain of module 3"
       LOCATION: 97..1482
OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: beta-ketoacyl ACP synthase of module PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 10723..20235
OTHER INFORMATION: /codon_start= 10723
OTHER INFORMATION: /function= "gene =eryA"
OTHER INFORMATION: /product= "orf3 encoding modules 5 & OTHER INFORMATION: /function= function = func
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KET: misc_feature
LOCATION: 10733..15165
OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: module 5" "approximate span of NAME/KET: misc_feature
LOCATION: 10831..12174
OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: beta-ketoacylACPsynthase domain of OTHER INFORMATION: beta-ketoacylACPsynthase domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 12379..13350
OTHER INFORMATION: /function= "approximatr span of
OTHER INFORMATION: acyltransferase domain of module 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 644.7026
OCHER INFORMATION: __function="approximate span of
OTHER INFORMATION: acyltransferase domain of module
                                                                                                                                                                            LOCATION: 1693. 2670
OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: acyltransferase domain module 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LCCATION: 4171..4428
LCCATION: 4171..4428
OTHER INFORMATION: acyl carrier domain of module 3"
FEATURE:
NAME/KEY: misc_feature
LCCATION: 4471..1072
COTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: module 4"
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LOCATION: 10225..10483
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: 9433..9984
COTHER INFORMATION: /function= "approximate span
OTHER INFORMATION: beta-ketoreductase of module
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
14062..14610
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LOCATION:
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2216 TCGGGGGGGATCGCGCTGCCCGAGCTGACCCCCGACCAGCTCCGGGAGTCGG 2275
                                                                                                        1244 accgctggatcgacgcggtcgtgaagacgatggccgccgaatccgacgacaaccgcgcgc 1303
                                                                                                                                                     /codon_start= |19
/function= "gene eryA"
/product= "eryA ORF2 encoding modules 3 & 4 for
6-deoxyerythronolide B"
                                                                                                                                                                                                                                                   APPLICANT: Kalz, L
APPLICANT: Kalz, L
APPLICANT: Donadio, J
APPLICANT: Malpine, J
TITLE OF INVENTION: Recombinant DNA Method for Producing
TITLE OF INVENTION: Brythromycin Analogs
CORRESPONDENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Edward H. Gorman
STREET: Abbott Laboratories D377/AP6D-2 One Abbott
STREET: Park Rd
CITY: Abbott Park
STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: 19.4470
OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: module 3"
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STRAIN: NRRL 238
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ATTORNEY/AGENT INFORMATION:
NAME: DANCKEY, ANGREAS M
REGISTRATION NUMBER: 32652
REFERENCE/DOCKET NUMBER: 4952.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-9396
TELEPHONE: 708-937-9396
TELEFERAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 20235 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONDUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION NUMBER: US/07/642,734C
FILING DATE: 17-JAN-91
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/07642734C Patent No. 5824513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
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LOCATION: 19..10722
OTHER INFORMATION: /c
OTHER INFORMATION: /F
OTHER INFORMATION: /F
OTHER INFORMATION: /F
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ORIGINAL SOURCE:
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US-07-642-734C-3
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1279 gecgaatecgaegaegaeaec---gegegetgetegeeegetggaeaegegaetggteege 1334
                                                                                                                                                          1335 gegegecgaggeggeactggeaceggtggeggeaegegeegetgeaggatgeegggegege 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       874 aacgcgcagatctgcgcgctcggctacggcacggtgttcaccgcgcccgcgatgttccat 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gegatggacaaccteggegtegegeatacctcacgegtctegegetegegatggeegag 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gegegggegetegaegtgetggtgeegetgegeeaegeegegtggggegegaacatgaae 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 SCGCYGSACCTCSRCCYCSWSMYWGMSMASGCGCACCAGCCSKYCATGKCGCCSTCKCWC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 CACGSCTGGGACGGCAATGSCSCCAMWGSCGYSCCCACWCCSATGCCCAAGAGGCTGGAM 254
      8119 TACGAACCCGAAGGCGACGACCCCCGCGCGCGCCCCCCACGGCGTCCTCTGGGCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: DELLAPORTA, STEPHEN L.
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FPLICATION NUMBER: US/08/440,856A
FILING DATE: 15-MAY-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 65.4; DB 2;
Pred. No. 0.00013;
; Mismatches 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 05463-20001.00
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 887-1517
TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVE. N.W.
                                                                                                                                                                                                                                                                                                                                                                        US-08-440 856A-9; Sequence 9, Application US/08440856A; Patent No. 5750873; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.1%; So
ilarity 36.6%; Pr
Conservative 86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 706141
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1288 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
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Best Local Similarity
Matches 328; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: D.C.
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1219 atgecegaatggeacacegagtegaacegetggategaegeggtegtgaagaegatggee 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7582 CACTACGACGCCTCGCGAGCCAGGCTACGAGTACGGACCGTCGTTCCAGGCCCTGCGA 7641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7642 GCCGCGTGGCGCAAGGACGACTCGGTCTACGCCGAGGTGTCCATCGCGGCGGACGAGGAA 7701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7702 GGTTACGCGTTCCACCCGGTGCTGCTCGACGCCGTGGCGCAGACGCTCAGCCTGGGCGCC 7761
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beta-ketoreductase domain of module 6"
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LOCATION: 16768..17721
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain of module
                                                               NAME/KEY: misc_feature
LOCATION: 14857..15114
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 5"
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OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: acyl carrier domain of module 6"
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LOCATION: 19492..20235
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/function= "approximate span
beta-ketoreductase of module
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Pred. No. 3.4e-05;
0; Mismatches 311;
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Best Local Similarity 47.1%;
Matches 283; Conservative
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LOCATION: 15166..20235
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CURRENT APPLICATION DATA:
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                                                                                                                                                      39,872
                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
TELEFAX: 317-276-3861
                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                        LENGTH: 1224 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Matches 228; Conservative
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                                                                  FILING DATE:
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; LOCATION:
US-08-924-847A-1
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                    GGGAAGGTGGCCATTGTSACSGGCGGSGCGMGSGGGATCGGSGAGGCSATCGTGMGGCTG 314
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COMPUTER: Eloppy disk
COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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GENERAL INFORMATION:
APPLICANT: Baltz, Richard H.
APPLICANT: Solenberg, Patricia J.
APPLICANT: Treadway, Patti J.
TITLE OF INVENTION: Glycopeptides Der NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis
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ANTI-SENSE: N
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; LOCATION:
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APPLICANT: Treadway, Patti J.
TITLE OF INVENTION: Glycopeptides Derived From Cloned Gene gtfD
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.0011
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40.0%; Pred. No. 0.0
tive 25; Mismatches
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/924,847A
                                                                                   Eli Lilly and Company
                                                                                             STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
TELEFAX: 317-276-3861
                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1224 base pairs TYPE: nucleic acid
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                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                 46285
                                                                                   ADDRESSEE:
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US-08-924-847A-3
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                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Baltz, Richard H.
APPLICANT: Solenberg, Patriola J.
APPLICANT: Treadway, Patri J.
TITLE OF INVENTION: Glycopeptides Derived From Cloned Gene gtfD NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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Pred. No. 0.0011;
0; Mismatches 279;
1287 cgacgacaaccgcgcgctgctcgcccg 1313
                                                765 CGCGAAGAUCGCCGUCGAGGUGAGCCG 791
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APPLICATION NUMBER: 08/924,847
                                                                                                                                                                     Sequence 1, Application US/09120052 Patent No. 6025174
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,
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Best Local Similarity 45.0 Matches 228; Conservative
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Query Match
Best Local Similarity
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ggccgagcccgacgtgctggaggcggccaaggcgacctggacccgcgacgccgcctggca 1046
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                              465 GGAAGAGCGTGCCCACCGGTTCGCGGAACGGTACGGGGAGACGCTCAACCGGCGGCGGCGGC 524
                                                                                              525 CGCGATCGGCCTGCCGCCGGTGGAGGACGTCTTCGGCTACGGCCACGGCGACCGGCCCAT 584
                                                                                                                                                                                                                                                                                      705 CGCCCACCGCCGCGCGCGCGCTTCGGCAGCTCGTCCGGGAAGGGGATCGCCGACGC 764
                                                                                                                                                                                                                   1047 gccgctgcgccgctacgtcgaggacacgctggtcgtcgccgatccggtcgagctgttcat
                                                                                                                                                  APPLICANT: Baltz, Richard H.
APPLICANT: Solenberg, Patricia J.
APPLICANT: Treadway, Patti J.
AITLE OF INVENTION: Glycopeptides Derived From Cloned Gene gtfD
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version #1.30
                                                                                                                                                                                                                                                                                                                               1287 cgacgacaaccgcgcgctgctcgcccg 1313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-10897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/924,847
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09120052 Patent No. 6025174 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
TELEFAX: 317-276-3861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1224 base pairs
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COMPUTER READABLE FORM:
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STRANDEDNESS:
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US-09-120-052-3
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APPLICANT: Tatsumi, Hiroki
APPLICANT: Eisaki, Nacki
APPLICANT: Eisaki, Nacki
APPLICANT: Horiuchi, Tatsu
APPLICANT: Nagahara, Ayumu
TITLE OF INVENTION: Pruvate Orthophosphate Dikinase Gene,
TITLE OF INVENTION: Orthophosphate Dikinase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: MEDLEN & CARROLL, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
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                                                           Gaps
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  Length 1224;
                                                         Indels
; Score 60.6; DB 5; I
; Pred. No. 0.0011;
25; Mismatches 279;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08941936 Patent No. 6054305
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  1.0%;
                                                      Matches 203; Conservative
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MEDIUM TYPE: Floppy
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TYPE: nucleic STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tgtgcgggccgccggcgatgatcgacgcgtgcatcacgacgctgatgcaggggcgcctgt 4791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158 ACGGTGGCATGCCCGATGGCTGGCGGAGAGATTGACGAGCACCTTGCCGCCTCGAGG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278 GAGCCAAGTTCTCGATGCCGGGCATGATGAAGGTCCTCAACATCGCCTCAACGACG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       398 GCCGGCTCATCCAGATGTTCGGCAAGACCGTCCTGGGCATCGACGGCGAGCTGTTCGAGA 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 AGCGGATGGGCAAGCGCCTGGGCCAGGCGGACGACCGTTGCTGGTCAGTGAGGTCGG 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 59.4; DB 5; Length 2
Pred. No. 0.0021;
0; Mismatches 646; Indels
                       HIRAKI-03009
                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Microbispora thermorosea
STRAIN: IFO 14047
             REFERENCE/DOCKET NUMBER: HIRAL TELECOMUNICATION INFORMATION: TELEPHONE: 415-705-4410
TELEPHONE: 415-705-4410
TELEFAX: 415-705-838
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2634 base pairs TYPE: nucleic acid STRANBEDESS: double
REGISTRATION NUMBER: 32,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 41.5%;
Matches 462; Conservative
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1..2634
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; LOCATION:
US-08-941-936-1
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4792 togagogogacatotatoaogagaagttoatotoggoggoogacgogaacagacgogca 485]
                                                                                                          gcccgctgttccggcgggtgtgacatggacgcgggccgcgtatgcgg----gacggtca 4906
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                                                     ACCCGCAGGCCTACCGCGAGCTCCTGGACATCATGGCGACCCTGGAGCGGCACTACCGCG 937
                                                                                                                                         938 ACCTGTGCGACATCGAGTTCACGATCGAGCGGGCAAGCTGTGGATGCTGCAGACCCGGG 997
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ZIP: 07470

COMPUTER READABLE FORM:
MEDIUM TIPE. Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/08/125,468
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STREET: One Cyanamid Plaza
CITY: Wayne
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Patent No. 5589385
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REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET UNBER: 31,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Kyan, Michael J.
APPLICANT: Lotvin, Jason A.
APPLICANT: Strathy, Nancy
APPLICANT: Fantini, Susan E.
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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EDNESS: single
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CORRESPONDENCE ADDRESS:
ADDRESSEE: American
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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COUNTRY: USA
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APPLICANT: Ryan, Michael J.
APPLICANT: Fyan, Michael J.
APPLICANT: Lotvin, Jason A.
APPLICANT: Strathy, Nancy
APPLICANT: Strathy, Nancy
APPLICANT: Fantini, Susan E.
TITLE OF INVENTION: Cloning of the biosynthetic pathway for
TITLE OF INVENTION: useful therein and tetracyline Formation and cosmids
TITLE OF INVENTION: useful therein
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                         ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,468
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: TSEVGOS, ESTELLE J
REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31,255-02
RELEPHONE: (201)831-3241
TELEPHONE: (201)831-3345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PATENTIN PC-DOS/MS-DOS SOFTWARE: PATENTIN RELEASE #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/474,933 FILING DATE:
Sequence 1, Application US/08474933
Patent No. 5866410
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            ZIP: 07470
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                      STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                     Wayne
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                                                                                                                                                                                                  3872 gatgetegatgeegeetgegeeagggeatetaeatteegeacgegtgetgteaeggget 3931
                                                                                                                                                                                                                                         2221 CAGCCTGACCGAGCGACTGCTGCACCGCCGGCGTCGACCGGGTCGGCAGCGTCGA 2280
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                                                                               . 9
                                           Length 30001;
                                     Score 59.2; DB 1; Length 3
Pred. No. 0.0035;
0; Mismatches 548; Indels
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                                       1.0%;
ilarity 42.2%;
Conservative (
                                                          Similarity
                                                          Best Local Sim:
Matches 404;
                                         Query Match
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Version #1.25

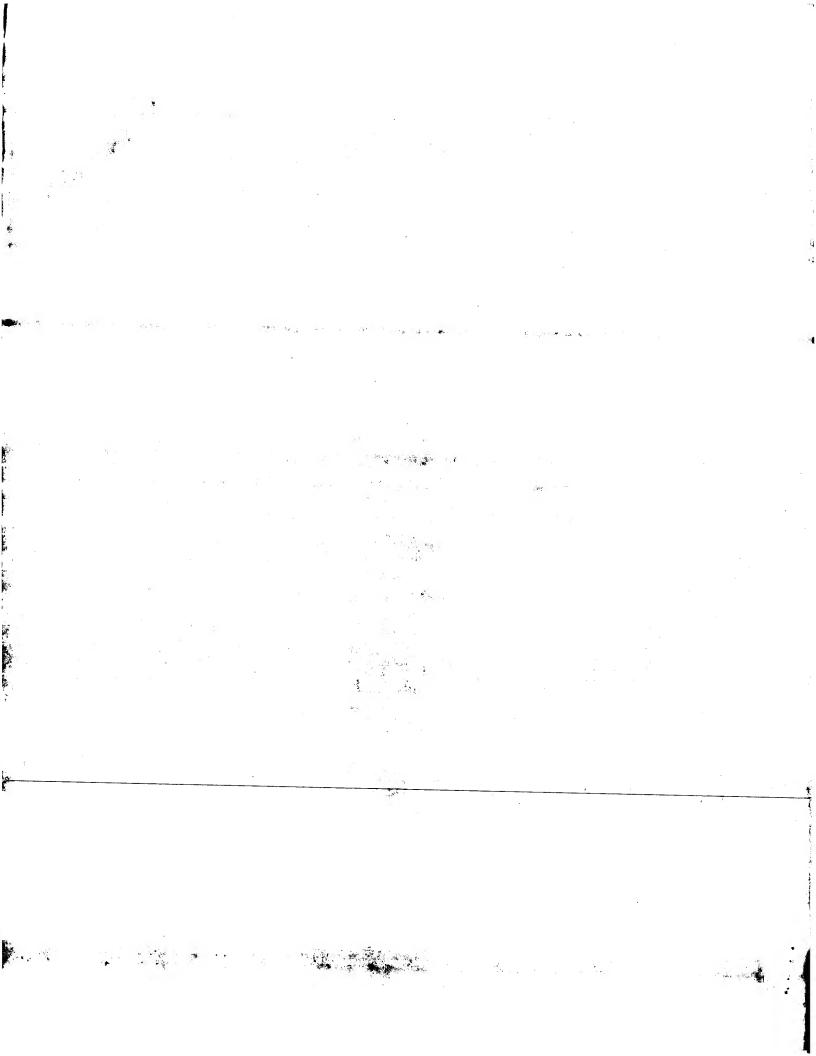
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                                                                                                                                                                                                                                                                 2161 GACACACGTCTTGACAACCGTGAACATCGGAATCCTGGCCCATGTCGACGCCGGTAAGAC
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6
                                                                                                                         Length 30001;
                                                                                                                      Score 59.2; DB 3; Length 3
Pred. No. 0.0035;
0; Mismatches 548; Indels
                      MOLECULE TYPE: DNA (genomic)
                                                                                                                         1.0%;
                                                                                                                      Query Match 1.0
Best Local Similarity 42.2
Matches 404; Conservative
linear
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RESULT 15 US-08-474-933-1

QQ	2461 GGTCATCTCCGCCGTGGAGGGCGTACAGGCCCAGACCCGGCTGCTGATGCGCACGCTGGT 2520
οy	4172 gatcogoctgaagctgtcgcagccgatccgcttccaggcgggccagtacgtgcagctcga 4231
QQ	2521 GAAACTGCGCATGCCGGTCATCCTTCGTCAACAACATCGACAGGATGGGCGCGCGC
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Οý	4526 cacgetggtetacggteagogeagogeaggagetetaetaecaegaegaatteegege 4585
qq	2881 CATGATGCCCTGGTCGACGGGATCACCAGGTGTTCCGGTCAATCACGGCGGCGCTCTCGG 2940
δλ	4586 gctggccgaacgccatccgaacttcacgtacgtgccggcgctgtccgaaggcgcaccgca 4645
qa	2941 GGGCACCCTCCGGGTACCGTGTTCAAGATCGAGGGGGGGG
ΟŊ	4646 cgcgggcgacgtcgcgcaagggttcgtgcacgacgtcgcgaaggcacatttcggcgg 4705
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δy	4706 cgacttctccgggcaccaggcgtacctgtgcgggccgccgcgatgatcgacgcgtgc 4763
qq	3061 CGACCAGGAGCGGTCACCGAGATTCCCGGCCGCACCACGGTGGTCGAGGTGTTC 3118

Search completed: September 26, 2000, 19:23:33 Job time: 12928 sec



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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Post-processing: Minimum Match 0%
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Listing first 45 summaries em_vi:* gb_htg1:* gb_htg2:* gb_in1:* em_ba1:* em_ba2:* em_hum1:* em_hum2:* gb_htg4:*
gb_htg5:*
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2: gb_ba2:*
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5: gb_pat:*
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10: gb_pri:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AB006479 Comamonas	AB024741 Comamonas	I24403 Sequence 1	L40033 Pseudomonas	AF026065 Ralstonia	AB031996 Ralstonia	D28864 Pseudomonas	X80765 P.putida ge	M60276 Pseudomonas	X79063 P.putida ge	AF012632 Ralstonia	AB016861 Burkholde	D85083 Acinetobact	Z36909 A.calcoacet	AB017631 Comamonas	AB016863 Comamonas	AB016860 Pseudomon	AB016859 Pseudomon	AB016857 Pseudomon	AB016854 Pseudomon	AB016858 Pseudomon	AF112137 Burkholde	U93090 Comamonas s	AF109307 Pseudomon
a	AB006479	AB024741	124403	PSETBMAF	AF026065	AB031996	PSEPHEAA	PPPHEHYD	PSEPHHYD	PPPHH	AF012632	AB016861	D85083	ACPHENOL	AB017631	AB016863	AB016860	AB016859	AB016857	AB016854	AB016858	AF112137	CSU93090	AF109307
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% Query Match	47.0	46.0	42.7	38.5	34.1	33.4	29.7	29.3	27.7	27.7	20.8	17.9	13.7	13.4	12.7	12.4	12.1	11.4	11.1	11.0	10.6	7.8	7.8	7.4
Score	2738	2681.6	2490.6	2244.8	1988	1949.2	1729.2	1708.8	1617.2	1616.6	1213.4	1043.4	799.6	779.2	740.8	723.8	707.4	9.599	646	643	617	455.4	451.8	431.2
Result No.	-	7	m	4	5	9	7	80	6	10	c 11	12	13	14	15	16	17	18	19	20	21	22	23	24

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M88806 Pseudomonas A8016862 Comamonas A8016856 Pseudomon A8016855 Pseudomon AF228346 Acinetoba X59790 Putida td U20258 Pseudomonas U47111 Burkholderi AF112136 Burkholderi AF112136 Burkholderi AF112136 Pseudomonas U38269 GDNA of alk E10607 Alkenemonoo E10696 Gene of alk U20258 Pseudomonas AF065891 Ralstonia M64747 Pseudomonas AF065891 Ralstonia M64747 Pseudomonas AB011575 Unidentif AB011572 Unidentif	Troylase component rygenase, complete aphk; catechol phenol hydroxylase commonadaceae; comamonadaceae; complete com	Adaptation and regulation of the genes involved in phenol degradation and regulation of the genes involved in phenol degradation and regulation of the genes involved in phenol degradation Microbiology 144 (Pt 10), 2895-2903 (1998) 99018839 Location/Qualifiers 1. 6298 /organism="Commonas testosteroni" //db_xref="taxon:285" //db_xref="aphk" //gene="aphk" //gene="aphk" //dcodor_start=1 //transl_table=11 //product="phenol hydroxylase component" //protein_de" Phanol hydroxylase component" //db_xref="Gi:845545" //translation="METSTLDLPVCDLTRRSVRVLQKRANGFVDFEFSVGWPELTVEL //gene="aphL" //gene="aphL"
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Pred. No. 4.2e-271;
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5341. .6285

/gene="aphB"

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Best Local Similarity 69.4%;
Matches 3937; Conservative
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3 B 4 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6	1950 GCCCATGGACAAGGCTTTCCCCTAAGACTTCCAAGATCCAAGATCCAAGAACATCAAGAACAACAATCAAGAACAACAATCAAGAAAAACAAAAAAAA	1952 caaqtgggtcgacccgttccgcctgacgatggatggtactggaaataccagggcgagaa 2011 	ggaaaagaagctgtacgcggtgatcgacgcggtcagcagaacaacgcgttcctcggcgt 2071	gagogacgccgctacatcaacgcgctgaagctgtcctccagggggtgacgccgctcga 2131 	2132 atacctcgcgcaccgcggcttcgcgcatgtcggcacttcaccggcgagggcgcgcg 2191 	catogogigocagaigoagiogatogacogagitgoggoaciaocagaocogaaqogaigo 2251 	gatgtcgacgtacaacaagttcttcaacgggttccatcactcgaaccagtggttcgaccg 2311 	cgtgtggtacctgtcggtgccgaagtcgttcttcgaggacgcatttcgtcggtcg	cgagttcctgaccgcggtcagcttctcgttdgaatacgtgctgacgaacctgctgttcgt 2431 	geogttcatgtcggggcgcgctacaacggtgacatgtcgaccgtcacgttcggcttctc 2491 	cgcgcagtcggacgaatcgcgtcacatgacgctcggcatcgaatgcatcaagttcctgct 2551 	cgaacaggacccggacaacgtgccgatcgtgcagcgctggatcgacaagtggttctggcg 2611 	2612 cggctaccggctgctgacgctggtcgcgatgatgactacatgcagcccaagcgcgt 2671	2672 gatgagctggcgcgagtcgtgggagatgtaccgagcagaacggcggcggctgttcaa 2731 	2732 ggatctcgcgcgctacggcattcgcgagccgaaggctggcaggacgcctgcgaaggcaa 2791 	2792 ggatcacatcagccaccaggcgttggtcgacgttctacggcttcaacgcggccttcggcgtt 2851 	2852 ccacacctgggtgccgaccgaagacgaaatggctggctgtcggcgaagtatcccgactc 2911 	2912 gttcgaccgctactaccgcccgcgcttcgatcactggggcgagcaggccaggccaggccag 2971	3031

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4137 4211 4197 4271 4250 4331	36	4451 4425 4511 4485 4571	4545 4631 4605 4691	4665 4748 4725 4808	4785 4868 4845 4928	4902 4988 4962 5048	02 10 16 14 22
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Comamonas testosteroni phcR, phcK, phcL, phcM, phcN, phcO, phcP and phcQ genes for regulator, phenol hydroxylase subunits and ferredoxin-like protein, complete cds.

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Comamonas testosteroni (strain:R5) DNA.
Comamonas testosteroni
Bacteria; Proteobacteria; beta subdivision; Comamonadaceae;
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Characterization of a high-affinity phenol hydroxylase from
Comamonas testosteroni R5 by gene cloning, and expression in
Pseudomonas aeruginosa PAOlc
                                                                                                                                                                                                                                                                                                                                                             caagcatgccgcctacaaggtcgagcacgacgccgatctggatgcgctgcagcagcgcat
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Direct Submission
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Teramoto, M.
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FEATURES

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KIHDWDKWEDPFRLTWDAYWRYGGEKEKKLYAVIEAFAONNGOLGYTDARYLABLKLF
IOGVVPLEYYAHRGFAHAGRHFTGAGARVAAQMQSIDELRHFGTETHALSNYNKYFNG
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69.5%; Pred. No. 2.2e-265;
Live 0; Mismatches 1604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="ferredoxin-like protein"
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Matches 3850; Conservative
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PSCWMLLGYASGYSSAFFRRPVFFKENGCSTCGHAHCLIEGRROUPEDDED

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Submitted (10-MAR-1999) to the DDBJ/EMBL/GenBank databases. I Teramoto, Marine Biotechnology Institute Co., Ltd., Kamaishi, Institute; Heita 3-75-1, Kamaishi, Iwate 026-0001, Japan (E-mail:mteramoto@kamaishi.mbio.co.jp, Tel:81-193-26-6537,
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1. (bases 1 to 9785)
Shields, M.S. and Francesconi, S.C.
Microbial degradation of trichloroethylene dichloroethylenes aromatic pollutants
Patent: US 5543117-A 1 06-AUG-1996;
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Matches 3329; Conservative
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from Pseudomonas sp. strain JS150
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                                                                                                                                                                     monooxygenase; phenol hydroxylase; subunit-terminal oxygenase compone; toluene monooxygenase.
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Pseudomonas sp.
Bacteria: Proteobacteria.
1 (bases 1 to 5029)
Johnson,G.R. and Olsen,R.H.
Nucleotide sequence analysis of gentoluene/benzene-2-monooxygenase from Appl. Environ. Microbiol. 61 (9), 33 96035667
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TITLE
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                                                                                                                                               Raistonia sp. E2 positive phenol-degradative gene regulator (poxR), phenol hydroxylase components (poxA, poxB, poxC, poxD, poxE, poxF), and ferredoxin-like protein (poxG) genes, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIEGVVRVTPLTVDINIAAGVYHGEFLWEDSFEGDVHRQMFGVAQAPVCWMQIGYATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 9511)
Watanabe, K. and Hino, S.
Direct Submission
Submitted (18-SEP-1997) Kamaishi Laboratory, Marine Biotechnology
Institute, Heita 3-75-1, Kamaishi, Iwate 026, Japan
Location/Qualifiers
1. 9511
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                                                                                                                                                                                                                                                                                                   Ralstonia sp. E2.
Ralstonia sp. E2
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="positive phenol-degradative gene regulator"
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                                                                                                                               20-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                          Ralstonia.
1 (bases I to 9511)
Hino, S., Watanabe, K. and Takahashi, N.
Phenol hydroxylase cloned from Ralstonia eutropha strain E2
exhibits novel kinetic properties
Wicrobiology 144 (Pt 7), 1765-1772 (1998)
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
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Similarity 66.0%;
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Best Local
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O O	2468	gtcgaccgtcacgttcggcttctccgcgcagtcggacgaatcgcgtcacatgacgctcgg 2527
Oy Dp	2528	catogaatgoatcaagttootgotogaacaggacooggacaacgtgoogatogtgoagog 2587
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Qy Dp	3188 7529	caactgcttcccgcccgatgcggacccggggggggttcgatccgctcgccgcgggt 3247
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18;

Gaps

Length 8654;

Score 1949.2; DB 1; Pred. No. 8.7e-191; 0; Mismatches 1803;

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Conservative

Matches 3452; Ouery Match Best Local S

442

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Similarity

33.4%; 62.8%;

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5962	3792 6	3852 (3912 o	3972 9	4032 6	4092 (4152 c	4206 0	4266 6	4326 g	4386 c	4446 1	4506 6	4566 1	4626 0	4686 g	4734 t	79
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                                                                                                                                                                                                                                                                                                                                                                   Direct Submission Submitted (07-MAR-1994) to the DDBJ/EMBL/GenBank databases. Masahiro Takeo, Himeji Institute of Technology; 2167 Shosha, Himeji, Hyogo 671-22, Japan (E-mail:takeo@chem.eng.himeji-tech.ac.j p. Tel:(792-67-4893, Fax:0792-6/7-4891)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MTVTNTPTPTFDQLTRYIRVRSEPEAKFVEFDFAIGHPELFVEL
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Molecular cloning and sequencing of the phenol hydroxylase gene from Pseudomonas putida BH
J. Ferment. Bioeng. 79, 485-488 (1995)
On Jun 1, 1995 this sequence version replaced gi:468465.
Sequence updated (24-May-1995) by:
Masahiro Takeo.
                                                                                                                                   A4, A5, A6] genes for phenol
                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma|subdivision; Pseudomonas group;
                                                                                                                07-FEB-1999
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3 (bases 1 to 6112)
Takeo,M., Maeda,Y., Okada,H., Miyama,K., Mori,K., Ike,M. and
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Pseudomonas putida (isolate:BH) DNA.
Pseudomonas putida
                                                                                                           PSEPHEAA 6112 bp DNA
Pseudomonas putida phe[A1, A2, A3,
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1 (bases 1 to 6112)
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                                                                                                                                                                                                                                                   SOURCE
                                                                                                                                 DEFINITION
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JOURNAL
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<u> </u>	1491	cagatctgcgctccggctaggtaggtgttcaccgcgcccgcgftgttcatgcgatg 939 	
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οy	1054	cgccgctacgtcgaggacacgctggtcgccgatccggtcgagctgttcatcgcgcag 1113	
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1 (bases 1 to 6343)
Herrmann, H., Muller, C., Schmidt, I., Mahnke, J., Petruschka, L. and
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Submitted (29-70U-1994) H. Herrmann, Ernst-Moritz-Arndt
Universitaet, Greifswald, Inst f Genetik und Biochemie, Jahnstr
15a, 17487 Greifswald, FRG
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Pseudomonas putida
Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
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5064 cgggccgatcagccgtgcccatgtgagcgcggaagaagaagaacgacggctacgcgttgc
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Pseudomonas putida strain H
Mol. Genet. 247 (2), 240-246 (1995)
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90 A A O A

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Matches 2756; Conservative
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Pseudomonas putida phenol hydroxylase (dmpKLMNOP) operon, complete
                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
                                                                                                                                                                                                                        1 (bases 1 to 5449)
Nordlund, I., Powlowski, J. and Shingler, V.
Complete nucleotide sequence and polypeptide analysis of
multicomponent hydroxylase from Pseudomonas sp. strain CF600
91072230
                                                                                                                     phenol hydroxylase.
Pseudomonas putida (strain CF600) plasmid DNA.
Pseudomonas putida
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                    LOCUS
DEFINITION
                                                                                 ACCESSION
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KEYWORDS
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TITLE
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Indels 100;

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CTGCTGCGCTGCCTGCTGCCGCTGCCGCATGCCGAGCTGGGCGCCCAACATGAATAACAGC	cagatctgcgcgctcggctacggcacggtgttcaccgcgcgccgcagatgttccatgcgatg	GACCCA	tctcg-	CATCGG	gacccg 		1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	40	SATGTA	gctgac	SCTCAC	gaagac	CAAGAC	ctggtc 	TGGGA	2999cg Ggraf	14100	catege Tri	, i	TACAT	Saacc	THE I	Tot day	CTGGA	Jctcca	- AATGCT	gctgag	 CTCGA	Jacacg		gcctc 	SATCTG	Jaggge 	200000
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Oy Db	3931	tgtgcggcacctgcaaggtcgccgtgctcgacggcgagaccgatcccggcgatgcgaacc 3990 	
çy D	3991 4532	ogttogogctgatggatttogagcgogaggaaggcaaggc	
à é	4051	tgcaggccgacaccgtgatcgaggccgacgtcgacgaggagccggatgcggaaatcatcc 4110 	
7 YO	11 2	orginesarciogisalicandecearciteariocearciteariocearcitearitecires (403)	

2 (bases 1 to 5700) Ng.L.C., Shingler,V., Sze,C.C. and Poh,C.L. Cloning and sequences of the first eight genes of the chromosomally encoded (methyl) phenol degradation pathway from Pseudomonas putida Ng,L.C. Direct Submission Submitted (15-APR-1994) L.C. Ng, National University of Singapore, Dept of Microbiology, Lower Kent Ridge Road, Singapore 0511, PPPHH 5700 bp DNA BCT 23-OCT-1995 P.putida genes for phenolhydroxylase and ferredoxin like protein. X79063 5062 Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group; cgagecegegetegategeggaeetgetegeaageggegteaeegegeegateaege tettegtgegtegeteggeegeggeegatgatetteatggeeggegggteggggetgt tggtctacggtcagcgcagcgcaggagctctactaccacgaagttccgcgcgctgg cgatccgcctgaagctgtcgcagccgatccgcttccaggcgggccagtacgtgcagctcg phenol hydroxylase 5363 CCGATGGGCCGGCGAGAGCAGCC 5386 ccgacgcgcaacagacgcgcagcc 4854 ferredoxin-like protein; Pseudomonas putida. Pseudomonas. 1 (bases 1 to 5700) GI:483477 putida Pseudomonas SINGAPORE 2 (bases x79063.1 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM 4772 5123 RESULT 10 5003 REFERENCE AUTHORS TITLE 4171 4825 4411 4471 4531 4591 4831 REFERENCE AUTHORS TITLE JOURNAL 4291 g Q g q ò g δ g ò g ò g Qγ Q ò ద δ qq δ δ δ Ω ò q

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EFINITION Ralstonia pickettii crpD, crpC, crpB, and crpA genes, complete cds. CCESSION AF012632
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Med. Sci. II, Ann Arbor, MI 48109-0620, USA
Location/Qualifiers
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RIFMKTLIPMLCQTCQIPMLFFDEMAMLSAKYPDSFDRYYRPRFDYWGEQARKAGN
345 C 203 t
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Submitted (12-AUG-1998) to the DDBJ/EMBL/GenBank databases.
Hiroyuki Futamatu, Marine Biotechnology Institute, Microbiol
Consortia Research Group; 3-75-1 Heita, Kamaishi, Iwate 026-0001,
Japan (E-mail:hfutamata@kamaishi.mbio.co.jp, Tel:81-193-26-6544,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (sites)
Futamata, H., Watanabe, K., Suda, F. and Harayama, S.
Unique primary structure found in phenol hydroxylases Exhibiting high affinity towards trichloroethylene
Unpublished (1998)
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                                           GTGCATCAAGTTCATGCTGGAGCAGGACCCCGACAACGTTCCCATCGTTCAGCGCTGGAT
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                                                                                                                                                                                      Bacteria, Proteobacteria, beta subdivision;
Burkholderia, Burkholderia cepacia complex.
1 (bases 1 to 1117)
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95.9%; Pred. No. 3.5e-98;
ive 0; Mismatches 46;
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Burkholderia cepacia (strain:E1) DNA.
Burkholderia cepacia
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partial cds, strain El.
ABO16861
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LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL MEDLINE FEATURES SOURCE	GDS	gene	gene	gene
Db 61 GGTGCTCGATCCCACAACACGCGTTCCTCGGCGTGACCGCGCGTACAT 120 Qy 2090 caacgcgctgaagctgttctccaggggacgcgcgcgctgaatacctcgggcaccgcg 2149	Qy 2270 gttcttcaacgggttccatcactcgaaccagtggttcgaccggtgtggtacctgtcggt 2329 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	2450 cgcctacaacggtgacatgtcgaccgtcacgttcggcttctccgcgcagtcggacgaatc	Oy 2630 gctggtcgcgatgatgatcgacatgcarcaagcgctgatgactgcGcGcTGCTCAC bb0 Oy 2630 gctggtcgcgatgatgatggactacatgcagcgcgcgtgatgactggcgcgagtc 2689 Illililililililililililililililililili	Qy 2810 ggcgtggtcgacgtctcaacgcttctaacgcggcctcggcgttccacacctgggtgccgac 2869	Oy 2990 gctgccgatgctgtgccagatcccgatgctgttcaccgagcggcaaccc 3049

RESULT D85083

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1.000 /translation="mTSKVYLALQDNDTSRYIIEAIEQDNPQATIQYLPAMIRVESTG ELVVRAETVSEKLGQNWDIQELQLMMITLGGNVDEDDDSFTLKWN" Direct Submission Submitted (07-MAY-1996) to the DDBJ/EMBL/GenBank databases. Toshio Omori, The University of Tokyo, Biotechnology Research Center; Yayoi 1-1-1, Bunkyo-ku, Tokyo 113, Japan (E-mail:aseigyo@hongo.ecc.u-tokyo.ac.jp, Tel:03-3812-2111(ex.3067), Fax:03-5802-3326) D85083 5552 bp DNA BCT 11-NOV-1997 Acinetobacter sp. gene for DMS oxygenase components, complete cds. D85083.1 G1:2605607
D85083.1 G1:2605607
DMS oxygenase component.
Acinetobacter sp. (strain:20B) DNA.
Acinetobacter sp. Marcebacteria; gamma subdivision; Pseudomonas group;
Moraxellaceae; Acinetobacter.
1 (bases 1 to 5552) 2 (sites)
Horinouchi,M., Kasuga,K., Nojiri,H., Yamane,H. and Omori,T.
Cloning and characterization of genes encoding an enzyme which
oxidizes dimethyl sulfide in Acinetobacter sp. strain 20B
FEMS Microbiol. Lett. 155 (1), 99-105 (1997) /codon_start=1 /transl_table=11 /product="DMS oxygenase component" /protein_id="BAA23332.1" /db_xref="G1:2605610" /transl_table=11 /product="DMS oxygenase component" /protein_id="BAA23333.1" 1. .5552 /organism="Acinetobacter sp." /strain="208" /db_xref="taxon:472" Location/Qualifiers /transl_table=11 384. .1385 /gene="dsoB" 384. .1385 /gene="dsoB" /codon_start=1 codon_start=1 75. .365 /gene="dsoA" 75. .365 1398. 1667 /gene="dsoc" 1726. .3261 /gene="dsoD" /gene="dsoA" 1398. .1667 /gene="dsoC" Omori,T. Direct St

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Dp	Dp	Dp	Dp	Dp	Dp	Dp	م	Dp	Dp	D		Dp	Db	Dp	Dp	Db	Db

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/gene="ORF1"
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/gene="ORF2"
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/gene="ORF4"
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/gene="ORF3"
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                 3991 GAAGCTGATGTGGATGAAGACGAGGATTTCTTAGGCTATTTAGTCCAAGACTACCAAGCC 4050
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Moraxellaceae; Acinetobacter.
1 (bases 1 to 5905)
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                                                             gacgicacgcgcatcgaacagcicacgccgaccatcaagicgatccgcctgaagcigicg
                                                                                                  4051 AAAGTCATTGAAATAACGGATTTATCGCCGACGATTAAAGGTGTTCGACTTCAACTTGAT
                                                                                                                                              cagccgatccgcttccaggcgggccagtacgtgcagctcgagattcccggcctcgggcag
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Schirmer, F.
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DLNMSQTELWKGLEYLTDAGQANELGLLAAGLGLEHYLDLRADEADAKAGITGGTPRT
EGPLYVAGAPESVGFARMDGGSESAHVDALIEGNVTDTAGQIIPMAKVEIWHANSL
GNGYSFPGSAFNLRRSIFTDTQGQYIAQTTMPVGYGCPPGGTTQALLNLLGRHGNR
PSHVHFVSABGYRKLTTQFNIEGDKYLWDPAFATRDGLIATALDVTDLAKIKGYNL
NKAFKHIKFNFQLVQDADQVPLQRLIVVE"

1199 c 1243 g 1647 t
                                                                              /translation="wtvQaTvEkYQFEPLDLQQNYGENMLLFIGWDHHTLFCSAHAFV
VSPKQSLQALIDGQ1QAGFEQHPDFKHIDWSKVEFRLNRNLLQADFSKSLEDLGFDHR
                                                                                                                                                                                                                                                                 ODYQAKVIEITDLSPTIKGVRLQLDRPMQFQAGQYINIQLPNIEGTRAFSIANTPSDK
LIEEHJIRKYGGAARTYVHDELSVGBEMALSGPYGQFPVRKSDQQWYIFTAGGSGSLS
SLOSMILDLLEHGDDRITIILFGGPRRDYAELYNREKFBYPDRYYIPARPPE
DQWTGFTGYVHEAVANYFENKCSGHKAYLCGPPPMIDDAISTLMQSRLFEKDIHFERF
                                                                                                                                                                                                                                         /translation="mSYQVTIEPAGTIIQVEEDQTILDAALRQGVWLPFACGHGTCGT
CKVQVTDGFYDVGEASPFALMDIEREENKVLACCCKPESDMVIEADVDEDEDFLGYLV
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                                                                                                                                                                                         /product="phenolhydroxylase component"
/protein_id="CAAB5385.1"
/db_xref="G1:535285"
                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/transl_table=11
/product="catechol 1,2-dioxygenase"
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Pred. No. 1.6e-71;
                                /product="phenolhydroxylase
/protein_id="CAA85384.1"
/db_xref="G1:535284"
/db_xref="SPTREMBL:Q43982"
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/db_xref="G1:535286"
/db_xref="SPTREMBL:Q43984"
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                                                                                                       SLLRFVTPDLAGYQGTHV" 3792. .4844
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/trans1_table=11
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                                                                                                             /gene="ORF6"
3792.
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/gene="ORF6"
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/gene="ORF7"
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Matches 2239; Conserv
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Submitted (11-SEP-1998) to the DDBJ/EMBL/GenBank databases.
Hiroyuki Futamata, Marine Biotechnology Institute, Microbiol
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Consortia Research Group; 3-75-1 Heita, Kamaishi, Iwate 026-0001,
Japan (E-mail:hfutamata@kamaishi.mbio.co.jp, Tel:81-193-26-6544,
Fax:81-193-26-6592)
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                                                                                                   Futamata, H., Watanabe, K. and Harayama, S. Mique primary structure found in phenol high affinity towards trichloroethylene Unpublished (1998)
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Search completed: September 26, 2000, 19;18:59 Job time: 12687 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

September 26, 2000, 15:50:55; search time 153.15 Seconds (without alignments) 9520.858 Million cell updates/sec Run on:

US-09-430-029-1 5828 1 galcatticatcaaatgcgc......tcggcccgggcaacacgatc 5828 Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

311585 seqs, 125096042 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_36:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

_	Infected cell prot	The nucleotide seq	Sorghum bicolor (L	Streptomyces prist	GtfC gene from Amy	snbR gene encoding	S. clavuliqerus cl	Tylactone synthase	Sequence encoding	Neomycin phosphotr	Maize nitrite redu	Hybrid srmG/tylG O	
	V10362	V68520	V57472	T58553	V60557	064206	091580	T80413	N50472	V42917	012000	T80415	
	ч	Н		7	Н	П	-	Т	-	Н	1	1	
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	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	
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	34	35	36	c 37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT T44457	-1	
74 74	T44457 standard; T44457:	DNA; 9785 BP.
29	1997	(first entry)
DNA	encodin	g toluene ortho-monooxygenase.
ÄÄ	down;	CCE; degradation; ss.
D S	Pseudomonas cepacia	cia strain PRI-23.
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		ct= tomA0
		/note= "no start or stop codons included; encodes
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Ħ	misc_difference	.3866
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		sl_except= (51165117, aa:Ala)
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cds	v	57506030
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Microorganisms transformed with P. cepacia PRI-23 Tom enzyme gene -
T are useful for degradation of chloro; aliphatic cpds. and aromatics
Sclaim 2; Column 19-28; 25pp; English.
The present sequence, isolated from peredomonas cepacia strain PRI-23, includes the gene(s) encoding follower ortho-monoxygenase, designated from. The Tom gene is present on a large self-transmissable plasmid denoted prow. The rayme is capable of degrading trichlorocthylene (TCE), a hazardous pollutant. The prow plasmid is transmissable and expressable in other bacteria, thus many bacteria can be genetically altred to constitutively degrade TCE, esp. in blorocactors or recentantmated environments. P. cepacia PRI-23 contg. prow does not need exogenous chemical inducers and is capable of functioning under a diverse set of conditions. Also it does not require an inducer that is a co-substrate for the enzyme required to break down TCE, in effect, it is consubstrate for the enzyme required to break down TCE, in effect, it is sequence 9785 BP; 2255 A; 2697 C; 2815 G; 2048 T;
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Pred. No. 0;
); Mismatches 1369; Indels 156;
/*tag- 1
/note- "apparent insertion"
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/*tag- "apparent insertion"
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70.38;
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Francesconi SC, Shields MS;
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Matches 3618; Conservative
                                                                                                                                  02-MAY-1991; US-694718.
15-DEC-1993; US-167457.
06-OCT-1994; US-319387.
                                                                                                                                                                                      (FRAN/) FRANCESCONI S C.
                                                                                                                                                                                                                                    WPI; 96-370640/37.
P-PSDB; W06800-05.
                                  misc_d1fference
                                                                                                                  02-MAY-1991;
02-MAY-1991;
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agcccgacgtgctggaggcggccaaggcgacctggacccgcgacgccgcctggcagccgc
                                                                                            agaacctcgcgctcgacggcctgctgtatccgctcgtctacgaccgcttcgtcgacgaac
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Qy Db	2189	gegeategegtgecagatgeagtegategaegagetgeggeactaceagaecgaaaegea 2 	
Qy Db	2249	tgcgatgtcgacgtacaacagttcttcaacgggttccatcactcgaaccagtggttcga 2308 	
Oy Db	2309	cogogtgtgtgtacttgtcggtgccgaagtcgttcttcgaggacgcgtattcgtcggggcc 2368 	
Qy Ob	2369	gttcgagttcctgaccgcggtcagcttctcgttcgaatacgtgctgacgaacctgctgt 2428 	
oy B	2429	cgtgccgttcatgtcgggcgcctacaacggtgacatgtcgaccgtcacgttcggctt 2488 	
O.Y	2489	ctcogcgcagtcggacgaatcgcgtcacatgacgctcggcatcgaatgcatcaagttcct 2548 	
oy Dp	2549	getegaacaggacceggacaacgtgecgategtgeagegetggategacaagtggttetg 2608 	
Qy Db	2609	gcgcgctaccggctgctgacgctggtcgcgatgatgatgatgactacatgcagcccaagcg 2668 	
Oy Db	2669 5064	cgtgatgagctggcgagtcgtgggagatgtacgccgagcagagcgcgcgc	
O _Y	2729	caaggatctcgcgcgctacggcattcgcgagccgaagggctggcaggacgcctgcgaagg 2788 	
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Oy Dp	2849	gttccacacctgggtgccgaccgaagacgaaatggctggc	
S G	5300	ctcgttcgaccgctactaccgcccgcgcttcgatcactggggcgagcagggccagggccgg 2968 	
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R 25-JUL-1997; 200625.

R P-PSDB; W98950, W98970, W98971, W98973, W98974, W98975, WPI; 99-197820/17.

R P-PSDB; W989696, W98970, W98971, W98973, W98974, W98975, WPI; 99-197820/17.

Rew encoding an aromatic cpd. oxidative decompsn. enzyme - useful in the fields of petroleum purification, chemical and drug industries of claim 1; Page 7-19; 35pp; Japanese.

Claim 1; Page 7-19; 35pp; Japanese.

Claim 1; Page 7-19; 35pp; Japanese.

Contenion PoxE, P
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Alcaligenes sp.
J11042088-A.
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Best Local Similarity 63.9%;
Matches 3549; Conservative C
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-	8244	QY 4028 QY 4028 11111 Db 8304 GTGCCA 7348 Da 8304	Cgcgcg 3067 Qy 4088	Catctt 3127 Qy 4148	3187 QY 4202 7528 Db 8484	og 4262 ogcggt 3247 Op 8544	Qy 4322 Qy 4322 Qy 4322 Qy 4322 Qy Qy Qy Qy Qy Qy Qy	9acaag 3367 Qy 4382 Db 8652	acaaac 3427 . Oy 4442 ARGTC 7709 . Db 8712	agtt 3487 Qy 4502 c	3547 Qy 4562 ctacta 3547 Db 8832 GTACGG 7826	3607 Qy 4622 g	291cg 367 Db 8952	3727 Qy 4727 8006 Db 9012	3787 QY 4787 3787 Db 9072	3847 Qy 4846	tacat 3907 09 4899	351 0183 QY 4941 Cga 3967 Db 9252	2y 5001 ctgcctgaa 4027 02 5001 ctgcctgaa
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ATGCCGCGCGCGCGCGTGCGCGTGTGCAAGGTCCGCATCGAATCGGGGCGCTACCGCA- 9370
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                 getegggeegateageegtgeecatgtgagegeggaagaagaagaaegaegetaegeet
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Phenol hydroxylase genomic DNA sequence.
Phenol hydroxylase; recombinant; phenol-assimilating microbe;
chlorinated; ethylene; decomposition; aerobical; ds.
Pseudomonas putida.
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/*tag= a
/gene= "phe2"
434. .1429
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Gene recombinant decomposing chlorinated ethylene - has a promoter inserted upstream of a phenol hydroxylase gene bisclosure; ageg 8-10; 12pp; Japanese.

Disclosure; ageg 8-10; 12pp; Japanese.

The present sequence represents a phenol hydroxylase genomic DNA sequence isolated from Pseudomonas putida strain KWI-9. The invention relates to a recombinant gene carrying a recombinant DNA in which a promoter is. Inserted upstream of a phenol hydroxylase gene decruposing activity.

The said phenol hydroxylase gene is a gene gp. consisting of chlorinated ethylene-decomposition promoting gene and chlorinated ethylene-certifier ethylene-decomposition of chlorinated composing gene gp. and carries said recombinant DNA on a chromosome.

The invention also provides a method for the decomposition of chlorinated ethylene using the above gene recombinant. The gene recombinant gives a high decomposition of chlorinated ethylene per microbe body. The method decomposition of chlorinated ethylene per microbe body. The method decomposition of chlorinated ethylene general services a chlorinated ethylene efficiently under aerobical condition.

Sequence 4800 BP; 897 A; 1579 C; 1534 G; 790 T;
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Pred. No. 0;
); Mismatches 1357; Indels 148;
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0
/*tag- b
/gene= "pheA"
/440. 1712
/*tag- c
/gene= "pheB"
/754. 3268
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/754. 360
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(KURK ) KURITA WATER IND LTD.
WPI; 99-161080/14.
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66.2%;
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Matches 2947; Conservative
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30-JUN-1997; 174996.
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(first entry)
putida phe operon.
triviene decomposition; pheZ; pheA; pheB; pheC; pheD; pheE; ethylene-decomposing gene; ds. acgrocogaccgacgtcgcggccaccggcgagatcgaactgaacgtgcggcag 4325 cogocggatcggggctgtcgagcccgcqtcgatgatcgcggacctgctcgca 4505 | 11111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 aggogcacogcacgoggoggogacgtcgcgcaagggttcgtgcacgacgtc 4685 acatttegg------cggcgacttcteegggcaceaggegtaeetg 4733 4147 regggeteggeaegggetacetgeaegageaactggegaegggegagegtg 4385 CACCATCCGCGCCATCTGGCTGCGCGTGAAGGGGGGGCGCCGCGCGCTGCTTC 4087 Location/Qualifiers 127. 345 /*tag= a /*roduct= phe2 434. 1429 /*tag= b /product= pheA 1440. .1712 /*tag= c /product= pheB 1754 .3268 /*tag= d /product= pheC rd; DNA; 4800 BP ||||| ||GTTC 4747 gttc 4862

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gccgcctggcagccgctgcgccgctacgtcgaggacacgctggtcgccgatccggtc
                                   GCGGCGTGGCAGCCGGCTGGTCGAGCGCAGCTTTGTGATCGAGGACTGGTTC
                                                                      gagctgttcatcgcgcagaacctcgcgctcgacggcctgctgtatccgctcgtctacgac
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                                                                                                                                                                                                                                chylene decomposing gene
Disclosure: Page 8-10: 12pp: Japanese
Disclosure: Page 8-10: 12pp: Japanese
This sequence represents the Pseudomonas putida strain KWI-9 pheZ, pheA, pheB, pheD, pheB coding sequence. The invention relates to a gene recombinant capable of decomposing chlorinated ethylene characterised by that a recombinant DNA in which a DNA fragment having a function of stopping transcription of a gene is inserted downstream of a chlorinated ethylene-decomposing gene derived from a microbe having chlorinated ethylene-decomposing activity is cariled on a chromosome. The gene recombinant gives a high decomposition of chlorinated ethylene body. It also decomposition of chlorinated ethylene per microbe body. It also decomposes chlorinated ethylene efficiently under aerobic condition.
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Best Local Similarity 66.2%;
Matches 2947; Conservative 0
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26-JAN-1999.
30-JUN-1997; 174997.
30-JUN-1997; JP-174997.
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MPI; 99-13559/12.

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MPI; 99-13
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16S ribosomal RNA; rDNA; microbe; oligonucleotide; probe; hybridisation; detection; primer; PCR; amplification; intergenic spacer region; ISR; oxygenase; ds.
Unidentified.
4326 gtgccgggcgggctcggcacgggctacctgcacgagcaactggcgacgggcgagcgcgtg 4385
                                                                                              4316 TICCTGGCGGCGGCTCGGGCTTGTCCAGCCCGGGCGCCATGATCCTGGACATGCTGGCT 4375
                                                                                                                                                                                                                                                                CTGCACGGCCTTTACGCCAATGGCGCGACCGCCCGACTTCCGTGGCCACAGGCCTATCTG 4615
                     cgcctgtcgggcccgtacggccgcttcttcgtgcgtcgctcggccgcggccgatgatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tgegggeegeeggatgategaegegtgeatéaegaegetgatgeaggggegeetgtte
                                                                                                                                                                                                                                                                                                                                                                                                                                                            gcgaaggcacatttcgg------cggcgacttctccgggcaccaggcgtacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X04453 standard; DNA; 652 BP. X04453;
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Gaps

3;

Length 652; Indels

Score 327.2; DB 1; Pred. No. 3.7e-48;); Mismatches 193;

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5.6%;

Best Local Similarity 69.9 Matches 456; Conservative

Similarity

Query Match

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2416
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                                                                                         ttcgtcggggccgttcgagttcctgaccgcggtcagcttctcgttcgaatacgtgctgac
                                                                                                                                                           catcaagttcctgctcgaacaggacccggacaacgtgccgatcgtgcagcggctggatcga
                                                                                                                                                                                                                                                                                 301 GATCAAGTTCCTCCTCGAGCAGGACGAGGCCAACGTCCCGATCGTCCAGGGCTGGATCGA
                                                                                                                                                                                                                                                                                                             caagtggttctggcgcggctaccggctgctgacgctggtcgcgatgatgatgactacat
                                                                                                                                                                                                                                                                                                                                       361 CAAGTGGTTCTGGCGCTCCTACCGCGTCACCGCACTCGTCGCCCAGATGCTCGACTACAT
                                                                                                                                                                                                                                                                                                                                                                                                                      2714 eggeggegegetgtteaaggatetegegegetaeggeattegegageegaagggetggea
                                                                                                                                                                                                                                                                                                                                                                                                                                      481 GCTCGCTCTTCGAGGACCTCGCCTTCTACGGCATCACGCCTCCGCGCCCACGTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2774 ggacgectgcgaaggcaaggatcacatcagccaccaggcgtggtcgacgttctacggctt
                                      ccagtggttcgaccgcgtgtggtacctgtcggtgccgaagtcgttcttcgaggacgcgta
                                                                                                      gaacctgctgttcgtgccgttcatgtcgggcgccgcctacaacggtgacatgtcgaccgt
                                                                                                                                                                                                                                                                                                                                                                  2657 gcagcccaagcgcgtgatgagctggcgcgagtcgtgggagatgta---cgccgagcagaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alkene monoxygenase subunit-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= amoD
/note= "encodes reductase"
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907. .1938
/*tag= a
/label= amoA
/note= "encodes alken
1935. .2288
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3805. .4833
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2300. 3805
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Q79569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reductase; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-AUG-1995
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ggcgctgtccgaaggcgcaccgcacggggggggggacgtcgccaagggttcgtgcacga 4681
                                CGTGCTCTCGGAGTCGTCGCCAGCCGACTGGCACGGCGAGACGGGCATGGTCACCGACGC 4673
                                                                                          CTTGCTGCGG------TGGCGCCCGAACTGGCGCATGACGTCTACCTGTGCGGGCC 4724
                                                                                                                                     Nocardia corallina can be cultured in a medium contg. Indole and will readily oxidise the indole yielding indigo into the culture medium. E. coli may also be transformed with the alkene mono-oxygenase gene and used as above to efficiently produce indigo by microbial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Page 5-10; 11pp; Japanese.
T17418 is the Nocardia corallina strain B-276 alkene mono-oxygenase gene. It encodes 4 protein products amob, amoB, amoC and amoD aderived from the 3 different reading frames of the operon. The gene is useful for the production of indigo via oxidation of indole.
                                                               gcccgcgatgatcgacgcgtgcatcacgacgctgatgcaggggcgcctgttcgagcgcga
                                                                                                                                                                                                                                                                                                               07-A0G-1996 (first entry)
Nocardia corallina alkene mono-oxygenase gene used for indigo p
Alkene mono-oxygenase; indole; indigo production; biosynthesis;
microbial oxidation; dye; ss.
Nocardia corallina B-276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prepn. of indigo by a microbiological method – by culturing a microbe having alkene monooxygenase activity to oxidise indole
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1934. .2288
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08-JUL-1994; JP-1796
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Best Local Simi
Matches 546;
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Sequence
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                                                                                                                                                                                                                                                                                                                                            3849 CGAGGACGGCGAGAGCCTCCTCGACGCCCCTGCGCAACAGCCTGCTCCTGAAGTACGG 3908
                                                                                                                                                                                                                                                                                                                                                                                                      GTGCAAGCACGGGGGCTGCGGGACCTGCAAGGTCCGGCTGCTCGACGACGACGTAGAGGA 3968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGCGCCAGCGTGCGCTGCACCGTGCACCATCGACGTCGAGCCGAGCGGCCTCACGGA 4085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAGGAGTTCTTCTCGGGCGACACCTCGCGCGAGTTCCAGACGGTCGTGGGCGGTGTCGA 4145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4434 CCTGATGATCGCCGGTGGGTCCCGCTCCCCCCCCTCTCGATGCTGCGAAACTTGGC 4493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ctcgatcgcgaacgcgccggccgacgtcgcggccaccggcgagatcgaactgaacgtgcg 4321
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                                                                                                                                                                                                                                                                                     Gaps
                                                                                   Claim 5; Page 5-10; 30pp; Japanese.

E.coli transformed with this DNA sequence are able to catalyse the epoxidation of alkenes. The DNA is derived from Nocardia corallina and comprises 4 open reading frames. ORFs amoA and amoC encode subunits 1 and 2 of the alkene monoxygenase enzymes and ORF amoD encodes a reductase capable of transferring electrons from NADH
                                                                                                                                                                                                                                                                                                                                                                                                                                     cggcgatgcgaacccgttcgcgctgatggatttcgagcgcgaggaaggcaaggcgctcgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4097 tgcggaaatcatcccggtc-----agggacttcgcggccgacgtcacgcatcga
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                                                                                                                                                                                                                                                                                     410; Indels
                                                                                                                                                                                                                                                       Length
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                                                                      Alkene mon:oxygenase and corresp. gene - useful for
                                                                                                                                                                                                            2103
                                                                                                                                                                                                                                                      Score 201; DB 1;
Pred. No. 1.6e-26;
0; Mismatches 410
                                                                                                                                                                                                            2060 C;
                                                                                                                                                                                           to a monoxygenase.
6379 BP; 1136 A;
                                                                                                                                                                                                                                                       3.4%;
                             (NIHA ) JAPAN ENERGY CORP.
                                                                                                                                                                                                                                                                                     Conservative
06-APR-1993; 105171.
06-APR-1993; JP-105171.
                                                        P-PSDB; R66213-R66216.
                                                                                                                                                                                                                                                                     Similarity
                                            95-009069/02
                                                                                                                                                                                                                                                                                   546;
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Best Local Si
Matches 546;
                                                                                                                                                                                              coenzyme
                                                                                                                                                                                                            Sequence
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Gaps 39; Length 6379; Indels Score 201; DB 1; I Pred. No. 1.6e-26;); Mismatches 410; ö Conservative

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29-JAN-1997
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 cgaggaaggacagacgatgetcgatgecgcgcqcqcgggcaatetacatteegeaege 3916
                                                                                                                                                                                                       gigcigcgcgacgcigcaggccgacaccgigaicgaggccgacgicgacgaggagccgga 4096
                                                                                                                                                                                                                                         GTGCGCCAGCGTGCCGCTGGAACCGTGCACCATCGACGTCGAGCCGAGCGGCCTCACGGA 4085
                                                                                                                                                                                                                                                                          tgcggaaatcatcccggtc-----aggggacttcgcggccgacgtcacgcgtcga 4147
                                                                                                                                                                                                                                                                                                         4086 GGAGGAGTTCTTCTCGGGCGACACCTCGCGCGAGTTCCAGACGGTCGTGGGCGGTGTCGA 4145
                                                                                                                                                                                                                                                                                                                                              acagctcacgccgaccatcaagtcgatccgcctgaagctgtcgc----agccgatccg 4201
                                                                                                                                                                                                                                                                                                                                                                          4146 GTTTCTCACGGGGGGACATCGCCCGGGTCCGGCTACGGCTAGAGCCGGGCGAGGAGTCGC 4205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4614 CGTGCTCTCGGAGTCGTCGCCAGCCGACTGGCAGACGGCGAGACGGCATGGTCACCGACGC 4673
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                   cttccaggcgggccagtacgtgcagctcgagattcccggcctcgggcagagccgcgcgtt
                                                                   gigotgicacgggctgiggcagcctgcaaggicgccgigctgacggcgagaccgaicc
                                                                                                                                     cggcgatgcgaacccgttcgcgctgatggatttcgagcgcgaggaaggcaaggcgctcgc
                                                                                                                                                                     ACCCGGGTCG---TCGTTCGCGCTGACGCCGGAGGACGCGCGAGAACGACGTGATCCTCGC
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BP.

T44457 standard; DNA; 9785 T44457;

T44457/C ID T4449 AC T444

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Microorganisms transformed with P. cepacia PR1-23 Tom enzyme geneare useful for degradation of chloro:aliphatic cpds. and aromatics claim 2; Column 19-28; 25pp: English.

The present sequence, isolated from Pseudomonas cepacia strain PR1-23, includes the gene(s) encoding toluene ortho-monooxygenase, designated bloreactor; pollutant; encodes nucleotide; encodes /transl_except= (6026. .6027, aa:Ala) /note= "apparent deletion of nucleotide; encodes οŧ Ala-Arg; apparent deletion /note= "no start or stop codons included; W06805" /transl_except= (5116. .5117, aa:Ala) /note= "apparent deletion of nucleotide" 5133. .5135 aa:Glx) DNA encoding toluene ortho-monooxygenase.
Oni pTOM; self-transmissable, constitutive; blorestoremy trichhoroethylene; TCE; degradation; ss Pseudomonas cepacia strain PRI-23. /transl_except= (4173. .4175, /note= "encodes W06801" 4198. .5753 deletion of /note= "apparent insertion"
6953. .6954 /*tag= k /note= "apparent insertion' /note- "apparent insertion" /note= "encodes W06802" 5116. 5117 /*tag= f "encodes W06800' "encodes W06804" Location/Qualifiers /note= "apparent cysteine and Stop /product= tomA0 /*tag= g /note= "encodes /product= tomA5 /product= tomA1 /product= tomA2 /product= tomA3 'product= tomA4 /pic. /note= "encc. .3866 nucleotides" .5753 Shields MS; 5750. .6030 /*tag= h 6185. .7245 /note= "enco 5224. .6225 2647. .2757 /*tag= a 6026. .6027 (first entry) *tag= 1 06-AUG-1995. 02-MAY-1991, 694718. 02-MAY-1991; US-694718. 15-DEC-1993; US-167457. (FRAN) FRANCESCONI S C. (SHIE/) SHIELDS M S. /note= "¿ W06803" /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= WPI; 96-370640/37 P-PSDB; W06800-05 misc_difference misc_difference misc_difference misc_difference misc_dlfference misc_difference misc_difference Francesconi SC, US5543317-A

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tom. The Tom gene is present on a large self-transmissable plasmid denoted prow. The enzyme is capable of degrading trichloroethylene (TCE), a hazardous pollutant. The prow plasmid is transmissable and expressable in other bacteria, thus many bacteria can be genetically altered to constitutively degrade TCE, esp. in bloreactors or TCE-contaminated environments. P. cepacia PRI-23 contg. prow does not need exogenous chemical inducers and is capable of functioning under a diverse set of conditions. Also it does not require an inducer that is co-substrate for the enzyme required to break down TCE, in effect, it it is subject to competitive inhibition.
                                                                                                                                                                                                                                                                                                                                                      8974 TCCTGCTCTTCGGTACCCTTCCTTCGACCGGTCGTATGCTGCAGTTCAACCTGCCGAGCG 8915
                                                                                                                                                                                                                                                                                                                                                                                             gocatgaactgcggctgttcgcgaagaaggcgctggtggggcaccgcggtcggctcgctga 5643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8737 TCATGAAGGAATGCCTGGACTTTTATCTGGCTGAGCAAGTTATGGTAGGTCCGGATAGTA 8678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9; Page 524; 19pp; Japanese.

The plasmid allows for the expression of metapyrocatechase under the control of a promoter/operator from the TOL plasmid of Pseudomonas putida, in an E.coli expression system with an ampicillin resistance marker. The 5'-terminal overhangs it's comipement by AATT- the 3'-terminal is overhung by TTAA.

Sequence 1240 BP; 272 A; 358 C; 357 G; 253 T;
                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tgctgatgtgcgaactgaacccggaggccgtgaaccgcgtcgaggagaacacgcgct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tcatggccgagtgtctcgacttccatctggccgagcaggtgatggtcggcccgggcaaca
                                                                                                                                                                                        2048 T;
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                                                                                                                                                                                                                                            DB 1; Length 9785;
                                                                                                                                                                                                                                                                               88; Indels
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20-JUN-1991 (first entry)
Portion of plasmid pSLMK1 encoding metapyrocatechase.
E.coll; ds.
                                                                                                                                                                                      2815 G;
                                                                                                                                                                                                                                          tch 2.4%; Score 137.2; DB 1 al Similarity 70.1%; Pred. No. 1.4e-15; 213; Conservative 0; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-NOV-1985.
15-MAY-1984; 097106.
15-MAY-1984; JP-097106.
15-MAY-1984; JP-097106.
(SAGA) SAGAMI CHEM RES CENTRE.
(CENG) CENTRAL GLASS KK.
(HODO) HODOGAYA CHEM IND KK.
(NIPS) NEPPON SODA KK.
WPI; 86-018108/03.
CYCLIC double-stranded DNA - for the prodn. of
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                                                                                                                                                                                    2697 C;
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J60241889-A
                                                                                                                                                                                        Sequence
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5543
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                                                                                                                                                                                                                                                                                                                                                                                                coggoggtoggcoaactgoggttoctgotgcoagoggcoatgaactgoggctgtto 5603
gttcttctgcggcatggcatgtgccggcacggcggcgatcaacaagtaaccaggaggaga 5243
                                                                                                                                                                                                                  445
                             86 GTACTITCGCCACGITGGCGGAAACAAACCIGACAACATGAACTAIGAAGAGGTGACGIC 145
                                                                                                                                                                                                                                                                                                                                                                                                                               446 AACAGTTGTGGCCGGCGCGTGCGCTTCCAGGCCCCCTCCGGGCATCACTTCGAGTTGTAT 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAGACAAGGAATATACTGGAAAGTGGGGTTTGAATGACGTCAATCCCGAGGCATGGCCG 565
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                                                                                GCCCTGGAACACTACGTCGAGTTGCTGGGCCTGATCGAGATGGACCGTGACGACCAGGGC
                                                                                                                                                                                                                                                                                   386 CTGGAGCGGGATCTGATGGCATATGGCTGTGCCGTTGAGCAGCTACCCGCAGGTGAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               circular double chain DNA having Pl promoter - contains meta-pyro-catechase and operator of Lambda phage.
Claim 7: Page 477-9; 30pp; Japanese.
The sequence is a component of the synthetic circular DNA which ma transform an E.coli host for the expression of metapyrocatechase. The metapyrocachase gene is linked to the 3/terminal of the PL promoter (N60853) having the amp r gene at it's own 3/terminal. The product is useful in production of important organic
                                                              ctcaccatgggtgtgatgcgtattggtcatgtcagtctgaaggtgatggacatggaagcg
                                                                                                                                 gcgctgcgtcattacgtacgcgtgctcggcatgcaggaaacgatgcgcgacgcggcggggc
                                                                                                                                                                                                                                                                                                                                ctgcagcagcgcatcgaagcgtacgggatcgcgaggatgctgcccgaaggcgcgtg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     626 TIGCCGGCGACCTATGACCTGTTCACCAAGGTGCTCGGTTTCTATCTGGCCGA 678
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(CENG) CEMPRAL GLASS KK.
(HODO) HODOGAYA CHEM IND KK.
(NIPS ) NIPPON SODA KK.
(TOYJ) TOYO SODA MFG KK.
(NISC ) NIESSAN CHEM IND KK.
WPI; 86-128931/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E.coli; catéchols; ds.
Pseudomonas putida mt-2.
J61067490-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-APR-1986.
07-SEP-1984; 187792.
07-SEP-1984; JP-187792.
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Pred. No. 6.2e-11; 0; Mismatches 292;

Length 1240;

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Score 109.8;

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Query Match 1.9 Best Local Similarity 50.3 Matches 298; Conservative

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Disclosure; p; Japanese.
Human GM-CSF derivs, have polypeptide fragment from N-terminal
promoter (N60853) having the amp r gene at it's own 3'terminal The product is useful in production of important organic
                                                                                                                                                   Length 2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Metapyrocatechase; GM-CSF; luekopaenia; osteomyelodysplasia; granulocyte macrophage colony stimulating factor; ds: Homo sapiens.
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                                                                                                                                                                         Pred. No. 6.3e-11;
0; Mismatches 292; Indels
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                                                                                                                                                   1.9%; Score 109.8; 50.3%; Pred. No. 6.36
                      The product is useful in production of in intermediates esp. catechol derivatives. See also N60853-4. 515 A; 531 C; sequence 2004 BP.
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13-SEP-1988; 229468.
13-SEP-1988; JP-229468.
(SAGA) Sagami Chem Res Centre.
WPI; 90-128250/17.
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Best Local Similarity 50.3
Matches 298; Conservative
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P-PSDB; R04097
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                                                                                       Gaps
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                                                                                                                                                                                                                                                            140 ATGAACAAAGGTGTAATGCGACCGGGCCATGTGCAGCTGCGTGTACTGGACATGAGCAAG
                                                                                                                                                                                                                                                                                                         gegetgegteattaegtaegegtgeteggeatgeaggaaaegatgegegaegeggggg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Circular double chain DNA having Pl promoter - contains meta-pyro-catechase and operator of Lambda phage.
Claim 7, Page 477-9; 30pp; Japanese.
The sequence is a component of the synthetic circular DNA which ma transform an E.coli host for the expression of metapyrocatechase.
The metapyrocachase gene is linked to the 3'terminal of the PL
                                                                                                                                                                                                                  ctcaccatgggtgtgatgcgtattggtcatgt'cagtctgaaggtgatggacatggaagcg
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                                            Length 1992;
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                                                                                    Indels
                                          Score 109.8; DB 1;
Pred. No. 6.3e-11;
                                                                                    Mismatches 292;
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Sequence encoding portion
                                                                                    Conservative
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07-SEP-1984; JP-187792.
                                                              Similarity
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                                                                                    Matches 298;
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Synthetic
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                                                                                                                                    61
                                                                                          Gaps
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Sequence of gene xylE encoding catechol 2,3 oxygenase (C2,3-O)
and a ribosome binding site.
Catechol; food industry; pharmaceuticals; cosmetics; disinfectant;
                                                                                                                                                           cyctycottcattacytacycytyctcyycatycayyaaacyatycygacycyygyca
                                                                                                                                                                                                                                               5425 atcaggoggggctcaagcatgccgcctacaaggtcgagcacgacgccgatctggatgcgc
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                                                                                                                                                                                                      5365 acgtctacctgaaatgctgggacgaatgggacaagtattcgctgatcctgtcgccgtccg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid vector for synthesis of catechol 2,3-oxygenase - carries XYL E gene and promoter for expression in gram-positive bacteria,
  of
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metapyrocatechase, bonded at its C-terminal to the N-terminal GM-CSF. Expression vectors pWGM1 and pWGM3 also contain the ta promoter/operator and the Sequence of metapyrocatechase. Sequence 924 Bp; 200 A; 266 C; 265 G; 193 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5722 acccggaggccggcgtgaaccgcgtcgaggagaacacgcgcttcatggccga 5773
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                                                                    Length
                                                                                         Indels
                                                                Score 109.6; DB 1;
Pred. No. 6.7e-11;
0; Mismatches 254;
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Zukowski M, Gaffney D, Speck D, Lecocq JP;
WPI: 83-742602/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N30167 standard; DNA; 958 BP
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Example; Fig 3; 66pp; French
                                                                  1.9%;
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/*tag= a
                                                               Query Match 1.99
Best Local Similarity 51.79
Matches 275; Conservative
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01-FEB-1982; FR-001574.
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P-PSDB; P30266.
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Human adenosine Al receptor antisense oligonucleotide fragment.

Human adenosine Al receptor antisense oligonucleotide fragment.

Antisense oligonucleotide; multiple target; antisense treatment;

impaired respiration; inflammation; lung disease;

pulmonary vasoconstriction; inflammation; allergic rhinitis;

acute asthma; allergy; asthma; impeded respiration;

respiratory distress syndrome; pain; cystic fibrosis;

pulmonary hypertension; pulmonary vasoconstriction; emphysema;

chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;

colon cancer; breast cancer; lung cancer; pancreatic cancer;

hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5701 gcctgctgatgtgcgaactgaacccggaggccggcgtgaaccgcgtcgaggagaacacgc 5760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 TGGATGAGGATGCTCTCCGGCAACTGGAGCGGGATCTGATGGCATATGGCTGTGCCGTTG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       546
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C2,3-O has uses in the food industry, the pharmaceutical industry, the cosmetics industry and as a disinfectant. It converts catechols to aldehydes. The inventors claim a plasmid vector carrying at least the xylE gene and a promoter for the expression of the gene in a foram positive bacteria, pref. Bacillus subtilis.

Sequence 958 BP; 211 A; 270 C; 276 G; 201 T;
                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 ATGAACTATGAAGAGGTGACGTCATGAACAAAGGTGTAATGCGACCGGGCCATGTGCAGC
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0
                                                                                                                                                                                                                                                                                           958;
                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                    Score 100.2; DB 1;
Pred. No. 2.7e-09;
0; Mismatches 283;
                                                                                                                                                                                                                                                                                1.7%;
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                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 48.8
Matches 270; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gcttcatggccga 5773
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17-SEP-1998; U19419.
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Disclosure; Page 37; 120pp; English.

Disclosure; Page 37; 120pp; English.

Callected against teleast 2 marks selected from target genes, coding and care directed against at least 2 marks selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, coding and non-coding regions, intron-exon borders, the formation codons, genomic flanking regions, intron-exon borders, the composition and all segments of RNAs encoding proteins associated with one corresponding to regions and all segments of RNAs encoding proteins associated with one corrected from sequences X55272-74. These multiple target colligonucleotides (specifically X55180-27) can be used for the antisense treatment of diseases and conditions of are those associated with impaired respiration and inflammation, inflammation, are those associated with impaired respiration and inflammation, allergic rhintis, acute asthma, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary usoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastasized to the lungs, including breast and prostate cancer.

Sequence 114955 BP; 6071 A; 29417 C; 35712 G; 21328 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 106575 CNNHNNNSGCGGGGCCGAGGCCAGGGGCCCNNHNNNSCGCGGGGCCGAGGCCAGGGGCCCNN 106516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HNNNSCCGCGGGGCCGAGCCAGGGGCCCNNHNNNSGCCGCGGGGCCGAGCCAGGGGCCCN 106456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106395 GCCCNNHNNNSCGGGCCGCGGGCCGAGGGCCCNNHNNNSCCGGGCCGCGGGCC 106336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106101 CCAGGGGCCCNNHNNNSGGGCAAGCCGGGCCGGGGCCGAGGGGCCCANHNNNSC 106042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106159 CGGGCCGCGG--GGCCGAGCCAGGGGCCC, INH NNNSGGCAAGCCGGGCCGCGGGGCCGAG 106102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106275 GGGCCGCGGGGCCGAGCCAGGGCCCNNHNNSAAG----CCGGGCCGCGGGGCCGAGCC 106220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glcatcgcgctcaaaccctacgacttcccggtgaaggatgccgtcgagaagtttccggcg 3493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cttcccgcccgatgcggacccgggcgcggagggcttcgatccgctcgccggggggtgctcga 3253
                                                                                                                                      in treatment of, e.g. pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106455 NHNNNSGGCCGCGGGGCCCAGGCCAGGGCCCNNHNNNSGGGCCGCGGGGCCGAGGC
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1.6%; Score 94.4; DB 1;
Best Local Similarity 33.8%; Pred. No. 3.1e-08;
Matches 656; Conservative 121; Mismatches 1145;
                                                                                                                              New antisense oligonucleotides used vasoconstriction
                                                  (UYEC-) UNIV EAST CAROLINA
                                                                                                       WPI; 99-229400/19
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106041 GGGCAAGCCGGGCCCGCGGGCCCGAGCCAGGGGCCCNNHNNNSGCGGGCAAGCCGGGCCGC 105982 GGGGCCGAGCCAGGGGCCCNNHNNNSGGCGGGCAAGCCGGGGCCGGGGGCCGAGCCAGGG 105922 105921 GCCCNNHNNNSGGGCGGGCAAGCCGGGCCGGGGCCCAGGGGCCCNNHNNNSCGG 105862 105742 CCGAGCCAGGGCCCNNHNNNSGGCCGGGCGGGCAAGCCGGGCCGCGG--GGCCGAGCCA 105685 105801 GGCC-GCGGGGCCGAGCCAGGGGCCCNHHNNNSGCCGGGCGGGCAAGCCGGGCCGCGGGG 105743 105684 GGGGCCCNNHNNNSGGCCGGGCGGGCGGCCAACCGGGCCGCGGGCCGAGCCAGGGCCCNN 105625 105624 HNNNSCGGGCCGGGCGGGCAAGCCGGGCCGCGGGCCCGAGCCAGGGGCCCNNHNNNSCCG 105565 105204 CGCCCNNHNNNSCGGCCCGGCCGCCGCCCCVNNHNNNSCGGCCCGGCCGGCGCCC 105145 Db 104966 HNNNSCGCCCGGCCGGCGCGCGCCCV----GCCCVCNNHNNNSCGCCCGGCCGGC 104912 cggatgcggaaatcatcccggtcagggacttcgcggccgacgtcacgcgcatcgaacagc 4152 4272 aggtcgaggaaggacagacgatgctcgatgccgcgctgcgccagggcatctacattccgc 105861 GCGGGCAAGCCGGGCCGCGGGGCCGAGCCAGGGGCCCNNHNNNSCCGGGCGGGCAAGCCG 3973 atcccggcgatgcgaacccgttcgcgctgatggatttcgagcgcgaggaaggcaaggcgc tegegtgetgeggeggetgeaggeegacacegtgategaggeegaegtegaegaggage 105564 GGCCGGGCGGAGCCGGGCCGCGGGCCGAGCCAGGGGCCCNHNNNSVGCGGAGCCV 4333 gcgggctcggcacgggctacctgcacgagcaactggcgacgggcgagcgcgtgcgctgt 105384 CGGNNHNNNSCGGCCCGGCCGGCGGCNNHNNNSCGGCCGGCCGCGCGCGCGNNHNNNSCGG cgaaggcgcaccgcacgcgggcggcgacgtcgcgcaagggttcgtgcacgacgtcgcgaa 105144 GCCCVGNNHNNNSCGGCCCGGC--CGGCGGCGCCCVGGNNHNNNSCGGCCCGGCCGGC 105086 GGGGGCCCVGGCNHNNNSCGGCCCGGGCGGCGCGCCCVGGCCCNHNNNSCGGCCC Db 105026 GGCCGGCGCGCCCVGGCCVNNHNNNSCGGCCCGGCCGGCCGCGCCCCVGGCCVGGNN 4811 cgagaagttcatctcggcggccgacgcgcaacagacgcgcagccgctgttccggcgggt ggacgagcgaaccatcatgagccaccaacttacca-tcgagccgctggggcgtcacgatcg acgcgtgctgtcacgggctgtgcggcacctgcaaggtcgccgtgctcgacggcgagaccg gecagtacgtgcagetegagatteeeggeetegggcagageegegegttetegategega gategacgegtgeateacgacgetgatgeaggggegeetgttegagegegacatetatea tcacgccgaccatcaagtcgatccgcctgaagctgtcgcagccgatccgcttccaggcgg acgcgccggccgacgtcgcggccaccggcgagatcgaactgaacgtgcggcaggtgccgg cgggcccgtacggccgcttcttcgtgcgtcgctcggccgcgcggcgatgatcttcatgg ccggcgggtcggggctgtcgagcccgcgctcgatgatcgcggacctgctcgcaag--cgg cgtcaccgcgccgatcacgctggtctacggtcagcgcagcgcgcaggagctctactacca 3794 4033 4273 4393 4453 4751 105981 3913 4093 4571 4213 4511 4631 4691 q g g g 쉽 a δŏ qq g d qq g ò ð ŏ ð ò g à ò ò ò qq οy δ g ò ò

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Vascourstitution

18 Disclosure; Page 37; 120pp; English.

The specification describes antisense oligonucleotides (X52869-X55271)

The specification describes antisense oligonucleotides (X52869-X55271)

The specification describes antisense oligonucleotides (and the last 2 mRNAs selected from trarget genes, coding and on-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-and, the 3'-end and the juxta-section between coding and non-coding cregions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides (specifically X55272-74. These multiple target creatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, and the first coding and allergies, asthma, impeded respiration, claiming the creatment of diseases, pulmonary vasoconstriction, inflammation, creatment distracts syndromers allergies, pulmonary converses.
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                                              Db 104911 GGGGGCCCVGGCCVGGGNHNNNSGGCCVGCGNNHNNNSVGGCCVGCGGNNHNNNSCV 104852
                                                                                                                                              104851 GGCCVGCGGNNHNNNSCCVGCCCVGCGGNNHNNNSCCCVGCCCVGCGGNNHNNNSGCCCV 104792
                                                                                                                                                                                                                                              Db 104791 GGCCVGCGGNNHNNNSCGCCCVGGCCVGCGGNNHNNNSGCGCCCVGGCCCVGCGGNNHNNN 104732
                                                                                                                                                                                                                                                                                                                           cggtgcgcaagctcgggccgatcagccgtgcccatgtgagcgcggaagaagaacgacg 5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human adenosine Al receptor antisense oligonucleotide fragment.
Antisense oligonucleotide; multiple target; antisense treatment;
impaired respiration; inflammation; lung disease;
pulmonary vasoconstriction; inflammation; allergic rhinitis;
acute asthma; allergy; asthma; impeded respiration;
respiratory distress syndrome; pain; cystic fibrosis;
pulmonary hypertension; pulmonary vasoconstriction; emphysema;
chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
colon cancer; breast cancer; lung cancer; melanoma; hepatic metastasis;
  gtgacatggacgcgggcgcgtatgcgggacggtcacgatcgcgcagaccgacgagcgct 4930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense oligonucleotides used in treatment of, e.g. pulmonary
                                                                                                                                                                                            4991 ttccggtcggctgcctgaacggcgggtgcggcgtgtgcaaggtgcgcgtgctgcgcggtg
                                                                                                  Db 104671 GGCCVGCGGNNHNNNSCGGCG 104651
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17-SEP-1998; U19419.
09-JUN-1998; US-093972.
17-SEP-1997; US-059160.
(UYEC-) UNIV EAST CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                 gctacgcgcttgcgtgccgcg
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4871
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If (bases 1 to 1618)
Is Leslie, A., Frisch, D., Yu, Y., Wood, T.C., Wing, R.A. and Wilkins, T.A.

An integrated analysis of the genetics, development, and evolution of the cotton fiber

Unpublished (2000)
On Jul 8, 1999 this sequence version replaced gi:5420635.

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Clemson University
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100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288

Email: rwingeclemson.edu

Frax: 864 656 4293

Email: rwingeclemson.edu
                                                               Spermatophyta;
Malvales;
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/clone="GA_Ea0012K16"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
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                                    Gossypium arboreum.
Gossypium arboreum
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Bagnoliophyta; eudicotyledons; Rosidae; eurosids II;
Malyaceae; Gossypium.
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44.8%; Pred. No. 8.2e-08;
tive 0; Mismatches 549; Indels
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Location/Qualifiers
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                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Malvacaes; Gossyplum.
1 (bases 1 to 1140)
Leslie,A., Frisch,D., Yu,Y., Wood,T.C., Wing,R.A. and Wilkins,T.A. An integrated analysis of the genetics, development, and evolution of the cotton fiber
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/clone-16A_Ea0012022"
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                                                                Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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Clemson University Genomics Institute
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High quality sequence stop: 1440.
Location/Qualifiers
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/lab_host="E. col1"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
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Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Malvales;
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                                                                                                                                                                        AW731135 1711 bp mRNA EST 20-APR-2000 GA_Ea0010A05 Gossyptum arboreum 7-10 dpa fiber library Gossyptum arboreum cDNA clone GA_Ea0010A05, mRNA sequence.
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/clone-i6a_Ea0010A05"
/clone-ib-"Gosspplum arboreum 7-10 dpa fiber library"
/clone_itye-"Fibers isolated from bolls harvested 7-10
                         5146 gacgicgaactcgaagiggccggccggctcaggaagccgttcttctgcggcaigt 5205
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1 (bases 1 to 1711)
Leslie, A., Frisch, D., Yu, Y., Wood, T.C.,
An integrated analysis of the genetics,
of the cotton fiber
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Pred. No. 1.6e-05;
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Location/Qualifiers
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/note="Vector: pBK-CMV;
858 c 573 g 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Gossypium
                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
On Jan 6, 2000 this sequence
Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                               100 Jordan Hall, Clemson, SC
Tel: 864 656 7288
Fax: 864 656 4293
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Clemson University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: rwing@clemson.edu
                                                                                                                                                                                                                              AW731135.1 GI:7628792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="AKA
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Similarity 46.4%;
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Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information pleases see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNSO091P 925 bp DNA GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR19016 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
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Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRi digestion of Drosophila DNA provided by the BDGP from the Isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           715 SKSSTBSSGSBSSGSSSSSTSSBBSCTSTSSSSSSSSSSTCSCCCCSYSYSSSTS 774
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Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 923)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMCGKKCGSTTBGSTTTTTTSSGSGYGKGCSSGSGBSCSCCSSCSCSSSSCSCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 925;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 14.6%; Pred. No. 3e-05;
Matches 57; Conservative 186; Mismatches 147; Indels
                                                                                                                                                                                                                     /organism="Drosophila melanogaster"
/db_xxef="Laxon:7227"
/clone_lib="RPCI-98"
/clone="BACR19D16"
                                                                                                                                                                                                                                                                                                                                                                                                                  1.3%; Score 73.2; DB 122;
14.6%; Pred. No. 3e-05;
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collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BAGs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Rosewell Park Cancer Institute in Buffalo. NY. The library is named RPCI-98 and was constructed by partial Ecorl digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://dacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster genome survey sequence T7 end of BAC # BACR14N09 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gacgggcgagcgcgtgcgcctgtcgggcccgtacggccgcttcttcgtgcgtcgctcggc 4429
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR19D16"
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12.8%; Pred. No. 3.3e-05;
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Spermatophyta;
Malvales;
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Mayaceae; Gossyptum.
1 (bases 1 to 1411)
Leslie,A., Frisch,D., Yu,Y., Wood,T.C., Wing,R.A. and Wilkins,T.A. An integrated analysis of the genetics, development, and evolution of the cotton fiber
On Jan 6, 2000 this sequence version replaced gi:6676845.
Contact: Wing RA
Colemson University
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="AKA"
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/db_xref="taxon:29729"
/clone="GA_EB0010117"
/clone=lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gcgagatcgaactgaacgtgcggcaggtgccgggcgggctcggcacgggctacctgcacg 4359
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472 g 96 t 21 others
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Pred. No. 8.4e-05;
0; Mismatches 432; Indels
                                                                                                                                                                                                                                                                                                                                                      100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Gossypium arboreum"
                                                                                                                                                                                                                                                                                                                                                                                                                Email: rwing@clemson.edu
High quality sequence stop: 1411.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E. coli"
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                             AW731189.1 GI:7628847
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Similarity 47.6%;
18; Conservative
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                                                                     Gossypium arboreum
Gossypium arboreum
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Genoscope.

Direct Submission

Submitted (02-UN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqreféqenoscope.cns.fr
- Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Barkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.frulfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gosegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila Plank Cancer Cantin 192; cn bw spp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Pred. No. 5.3e-05;
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/clone="BACR14N09"
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SM Gossypium arboreum.

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Malvales; Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

El (bases I to 1201)

E Leslie,A., Frisch,D., Yu,Y., Wood,T.C., Wing,R.A. and Wilkins,T.A.

An integrated analysis of the genetics, development, and evolution of the cotton fiber

Unpublished (2000)

L On Jan 6, 2000 this sequence version replaced gi:6676828.

Contact: Wing RA

Clemson University
Contact: Wing RA

Clemson University
Contact: Wing RA

Clemson University
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                                                                                                      4872 tgacatggacgcgggccgcgtatgcgggacggtcacgatcgcgcagaccgacgag-cgct 4930
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                                                     4871
                  527
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: 580 c 459 g 78 t 10 others
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                                                                                                                                100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 4293
ERA: 864 656 4293
Email: rwing@clemson.edu
High quality sequence stop: 1201.
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/organism="Gossypium arboreum"
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CNSO072Q 932 bp DNA GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14809 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ALO66742
ALO66742.1 GI:4945205
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  Length 1201;
                                          Indels
Score 70.8; DB 80;
Pred. No. 9.3e-05;
0; Mismatches 461;
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Query Match 1.2%;
Best Local Similarity 45.5%;
Matches 398; Conservative
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SOURCE

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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Malvales;
                                                                                                                                                                                                                                       Malvaceae; Gossypium.

I (bases 1 to 1626)
Leslie, A., Frisch, D., Yu, Y., Wood, T.C., Wing, R.A. and Wilkins, T.A.

An integrated analysis of the genetics, development, and evolution of the cotton fiber
of the cotton fiber
On Jan 6, 2000 this sequence version replaced gi:6676868.
AW731212 1626 bp mRNA EST 20-APR-2000 GA_Ea0010M15 Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA_Ea0010M15, mRNA sequence.
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654 g 135 t 45 others
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Pred. No. 0.00015;
0; Mismatches 453;
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100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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/organism="Gossypium arboreum"
                                                                                                                                                                                                                                                                                                                                                                                                                                  Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: rwing@clemson.edu
High quality sequence stop: 1626.
Location/Qualifiers
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670 c 65
                                                                                             AW731212.1 GI:7628871
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al Similarity 47.9%;
428; Conservative
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                                                                                                                                                                            Senoscope.

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
- Neb : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Aaron Mammoser in Pieter de Jóng's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the Isogenic strain y2: on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 932)
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                                                   Drosophila melanogaster
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                           fruit fly.
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Spermatophyta;
Malvales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW731160 1338 bp mRNA EST 20-APR-2000 GA_Ea0010E07 Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA_Ea0010E07, mRNA sequence.
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/db_xref="taxon:29729"
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/tissue_type="Fibers isolated from bolls harvested 7-10
gtgccggcgtgtccgaaggcgcacgcacgcggggcggcgacgtcgcgcaagggttcgtg 4676
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                                  GCGCAAGCGGCGACCGCGTGCGGGCACGGCGCGGCGGGGGCGCGGGCGCGGGC 793
                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. coli"
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597 c 619 g 68 t 8 others
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                                                                                                                                                                               cacgacgtcgcgaaggcacatttcggcggc.gacttctccgggcaccaggcgtacctgtg
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On Jan 6, 2000 this sequence version replaced gi:6676816.
Contact: Wing RA
Clemson University Genomics Institute
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; Rosidae; eurosids II;
Malvaceae; Gossyptum.
1 (bases 1 to 1338)
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Location/Qualifiers
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100 Jordan Hall, Clemson,
Tel: 864 656 7288
Fax: 864 656 4293
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AUTHORS
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4450 4510 4570 4749 4809 gaacgcgccggccgacgtcgcggccaccggcgagatcgaactgaacgtgcggcaggtgcc 4330 4390 4630 4689 4923 geteaegecegaceateaagtegateegeetgaagetgtegeageegateegetteeagge 4210 4984 cgcggcattccggtcggctgactgaacggcgggtgcggcgtgtgcaaggtgcgcgtgctg 5043. gctcgcgtgctgcgcgacgctgcaggccgacaccgtgatcgagggccgacgtcgacgagaga 4090 1312 eccelocedes de consecuencia de consecuenc .810 acgagaagttcatctcggcggccgacgcgcaaca----gacgcgcagccgctgttcc 4863 gagegetatgegtgegtgteeggegagtegetgetggeeggeatggegaaaeteggeegg 4983 902 842 605 545 gccggatgcggaaatcatcccggtcagggacttcgcggccgacgtcacgcgcatcgaaca 4511 cgtcaccgcgccgatcacgctcgtctacggtcagcgcagggggctcactacca cgaaggcgcaccgc-acgcgggcggcgacgtcgcgcaaggttcgtgcacgacgtcgcga 4750 tgatcgacgcgtgcatcacgacgctgatgcagggggggcgcctgttcgagcgcgacatctatc ggcgggtgtgacatggacgcggggccgcgtatgcgggacggtcacgatcgcgcagaccgac gggccagtacgtgcagctcgagattcccggcctcgggcagagccgcgcgttctcgatcgc gggcggctcggcacgggctacctgcacgagcaactggcgacgggcgagcgcgtgcgcct ggccggcgggtcggggctgtcgagcccgcgctcgatgatcgcggacctgctcgcaagcgg 1690 aggcacatttcggcggcgacttctccgggcaccaggcgtacctgtgcgggccgccgcga 19; Length 1338; Indels Score 69.6; DB 80; Pred. No. 0.00016; 550; 0; Mismatches 1.28; Query Match
Best Local Similarity 45.73
Matches 478; Conservative 4271 4451 4091 4924 4151 4211 424 g g qq qq á a δ g QQ δ g ò ά q ö δλ ŏ ōλ ò g ŏ δ g qq ŏ Db ŏ ŏ g ò g ò g

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1070 GGCGGCGGTGGTGCCGCGGGCGCGCGCGCGCGGGGCGCGCGCAGCGCAGCGGC 1011
                  4483 cgatgatcgcggacctgct-cgcaagcggcgtcaccgcgccgatcacgctggtctacggt
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100 Jordan Hall, Clemson, SC 29634, USA
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Malvales;
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                                                                                                                                           AW731188 1501 bp mRNA EST 20-APR-2000 GA_Ea0010115 Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA_Ea0010115, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cultivar="8400"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4189 cgcagccgatccgcttccaggcgggccagtacgtgcagctcgagattcccggcctcgggc 4248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4249 agagcogcogttctcgatcgcgaacgcgccgaccgacgtcgcggccaccggcgagatcg 4308
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27 others
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Gossypium arboreum.

Gossypium arboreum.

Gossypium arboreum.

Gossypium arboreum.

Eukaryota; Viridplantae; Embryophyta; Tracheophyta; Spe-
Magnolophyta; eudicotyledons; Rosidae, eurosids II; Mal-
Malvaceae; Gossypium.

E 1 (basses 1 to 1501)

E 1 (basses 1 to 1501)

An integrated analysis of the genetics, development, and of the cotton fiber

Unpublished (2000)

C on Jan 6, 2000 this sequence version replaced gi:6676844

Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                        version replaced gi:6676844
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45.1%; Pred. No. 0.00016;
tive 0; Mismatches 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V; Site_1: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
High quality sequence stop: 1501.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="E. coli"
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738 c 526 g 10
                              5044 cgcggtgcggtgcgcaagctcgggccg 5070
                                                    304 CGCGGCGGCCCCCCCCCCGCGCCCGG 278
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VERSION
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Gossyptum arboreum

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Majordeae; Gossypium.

E 1 (bases 1 to 1382)

S Leslie,A., Frisch,D., Yu,Y., Wood,T.C., Wing,R.A. and Wilkins,T.A.

An integrated analysis of the genetics, development, and evolution of the cotton fiber

Unpublished (2000)

On Jan 6, 2000 this sequence version replaced gi:6676856.

Contact: Wing RA

Clemson University Genomics Institute
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AW731200 GI:7628859
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cagogoagogoaggagototaccacgacgaattecggcgcgctggccgaacgccat
                                                                                                                                                         830 GCGACGGGGCCCGGGCGGCGCGCGCCTOACGTGAGGGGCGGCGGCGGCGGCGGCGGCGGCGCGCG
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                                                                                         /strain="ARA"
/culturar=8400.
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/clone="GA__Ea0010K15"
/clone="GA__Easypium arboreum 7-10 dpa fiber library"
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dpa"
                                                                                                                                                                                                                                                                                                                                                                                                                              4313 gaacgtgcggcaggtgccgggcgggctcggcacgcacgagcaactggcgac 4372
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13 others
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Pred. No. 0.00024;
0; Mismatches 493;
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119 t
                                                                              /organism="Gossypium arboreum'
                        Email: rwing@clemson.edu
High quality sequence stop: 1382.
Location/Qualifiers
                                                                                                                                                                                                  r: pBK-CMV;
551 g 11
                                                                                                                                                                                    coli"
                                                                                                                                                                                    /lab_host="E. c/note="Vector:
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al Similarity 43.7%;
385; Conservative
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               4293
                                                                1, .1382
Tel: 864 6
Fax: 864 6
Email: rwi
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Gossyptum arboreum.

Gossyptum arboreum.

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnollophyta; eudicotyledons; Rosidae; eurosids II; Malvales;

Malvaceae; Gossyptum.

1 (bases 1 to 1622)

Leslie,A., Frisch,D., Yu,Y., Wood,T.C., Wing,R.A. and Wilkins,T.A.

An integrated analysis of the genetics, development, and evolution of the cotton fiber

Unpublished (2000)

On Jan 6, 2000 this sequence version replaced gi:6676789.
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                                                                           gegaaacteggeeggeggeatteeggteggetgeetgaaeggegggtgegggegtgtge 5028
                                                                                                                                4209 gegggccagtacgtgcagctcgagattcccggcctcgggcagagccgcgcgttctcgatc 4268
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gcgaacgcgccggccgacgtcgcggccaccggcgagatcgaactgaacgtgcggcaggtg 4328
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801 c 493 g 112 t 94 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 68.8; DB 80;
Pred. No. 0.00024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 552;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Gossypium arboreum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clemson University
100 Jordan Hall, Clemson, SC 29634,
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 1622.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cultivar="8400"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW731133.1 GI:7628790
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/clone="GA_Ea0010005"
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/tissue_type="Fibers isolated from bolls harvested 7-10
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509 c 727 g 147 t 5 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1467;
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Pred. No. 0.00026;
0; Mismatches 596;
On Jan 6, Zuvv L.L. Contact: Wing RA Clemson University Genomics Institute Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 4293
Email: rwing@clemson.edu
High quality sequence stop: 1467.
Location/Qualifiers
                                                                                              USA
                                                                                                                                                                                                                                                       /organism="Gossypium arboreum"
                                                                                                                                                                                                                                                                                               /cultivar="8400"
/db_xref="taxon:29729"
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Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Malvales;
Malvaceae; Gossypium.
1 (bases 1 to 1467)
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GA_Ea0010005 Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_Ea0010005, mRNA sequence.
    ggcgtcaccgcgccgatcacgctggtctacggtcagcgcagcgcaggagctctactac 4568
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VERSION KEYWORDS

SOURCE ORGANISM

AUTHORS TITLE

REFERENCE

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4402 acggccgcttcttcgtgcgtcgctcggccgcgcggcgatgatcttcatggccggcgggt 4461
                                                                                                            4639 caccgcacgcgggggggggcgtcgcgcaagggttcgtgcacgacgtcgcgaaggcacatt 4698
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. sp_virus:*
sp_vertebrate:*
sp_unclassified:*

052171 pseudomonas 052162 pseudomonas 043979 acinetobact 032429 acinetobact 087802 pseudomonas 051943 burkholderi 069182 alcaligenes 053025 nocardia co 092et3 xanthobacte 007072 burkholderi 006117 methylocyst 013462 emericella mus musculu mus musculu ralstonia s pseudomonas 030592 burkholderi pseudomonas comamonas Description Q9wul9 Q9wum0 09znp6 052570 084959 SUMMARIES 013462 P78622 Q9WUL9 Q9WUM0 030592 092NP6 082870 084959 0852171 0652162 043979 087802 087802 069182 069182 006117 DB Query Match Length 342 333 333 333 342 343 341 341 395 1092 567 1101.5 1021.5 832 778 832 770.5 640.5 222.5 193 193.5 1179.5 1179.5 1179.5 1105.5 1105.5 Score Ň .

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LEAAKATWTRDAAWQPLRRYVEDTLVVADPVELFIAQNLALDGLLYPLVYDRFVDERIAL

LDVLVPLRHAAWGANMNNAQICALGYGTVFTAPAMFHAMDNLGVAQYLTRLALAMAEPDV

EGGSAVAMLTAFMPEWHTESNRWIDAVVKTMA----AESDDNRALLARWTRDWSARAEAA 296

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ID	030592	PRELIMINARY;	PRT;	335 AA.		
AC	030592;					
DΙ	01-JAN-1998 ((TrEMBLrel. 05,	Created)			-
DŢ	01-JAN-1998	(TrEMBLrel. 05,		Last sequence update)		
DŢ	01-JAN-1998	(TrEMBLrel. 05,		Last annotation update)	(e)	
DE	-			•		-
GN	CRPB.					
SO	Burkholderia	Burkholderia pickettii (Pseudomonas pickettii).	ndomonas	pickettii).		_
ပ္ပ	Bacteria; Pro	Bacteria; Proteobacteria; beta subdivision; Burkholderia group;	eta subdi	vision; Burkh	olderia group;	-
ဗ	Ralstonia.				,	
RN	[1]					-
RP	SEQUENCE FROM N.A.	M N.A.				
RC	STRAIN=PKO1;					-
RA	OLSEN R.H., I	OLSEN R.H., KUKOR J.J., BYRNE A.M., JOHNSON G.R.;	VE A.M.,	JOHNSON G.R.;		-
RL	J. Ind. Micro	J. Ind. Microbiol. 0:0-0(1997).	37).			-
DR	EMBL; AF0126	EMBL; AF012632; AAB67106.1; -	٠,٠			
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ALIGNMENTS

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_12:*

Database

sp_archea:*
sp_bacteria:*
sp_fung1:*
sp_human:*
sp_invertebrate:*
sp_namma1:*

sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:*

Gaps

Length 336;

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241

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LDVLVPLRHAAWGANMNNAQICALGYGTVFTAPAMFHAMDNLGVAQYLTRLALAMAEPDV 180
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                                                                                                                                                                                                                                                                                                                       61 PSRSAIRMANWYALKDPRQFYYASWATTRARQQDAMESNFEFVESRRMIGLMRDDVAARA 120
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                                                                                                                                                                                                                                                        1 MTIELKTVDIKPLRHTFAHVAQNIGGDKTATRYQEGMMGAQPQENFHYRPTWDPDYEIFD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOHNSON G.R., OLGEN R.H.;
"Nucleotide sequence analysis of genes encoding a toluene/Denzene-2-monoxygenase from Pseudomonas sp. strain JS150.";
Appl. Environ. Microbiol. 61:3336-3346(1995).
EMBL; L40033; AAA88457.1; -.
SEQUENCE 336 AA; 37042 MW; E4D0F654 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGGSAVAMLTAFMPEWHTESNRWIDAVVKTMA----AESDDNRALLARWTRDWSARAEAA
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Proteobacteria; beta subdivision; Burkholderia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N.;
Ralstonia eutropha strain E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 331;
                                                                                                                                                                       Score 1021.5; DB 2; Lens.
Pred. No. 1.2e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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SEQUENCE FROM N.A.
MEDLINE 99361023.
HINO S., WATANABE K., TAKAHASHI N.;
Phenol hydroxylase cloned from Ralstonia eutroph novel kinetic properties.";
Microbiology 144:0-0(0).
EMBL; AF026065; AAC32453.1; -.
SEQUENCE 331 AA; 37592 MW; F273FAAO CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
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ilarity 50.0%; Pred. No. 5e-61;
Conservative 49; Mismatches 1
                                                                                                                                                                                                                       40; Mismatches
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01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
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Best Local Similarity
Matches 166; Conserv
SEQUENCE FROM N.A.
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Ralstonia s
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Best Local S
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Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                  01-WAY-1999 (TrEMBLrel. 10, Created) | 01-WAY-1999 (TrEMBLrel. 10, Last sequence update) | 01-WAY-1999 (TrEMBLrel. 10, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
ALPHA SUBUNIT-TERMINAL OYGENASE COMPONENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.9%; Score 1101.5; DB 2; 62.9%; Pred. No. 3.1e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78;
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EMBL; AB006479; BAA34170.1; -.
SEQUENCE 330 AA; 37138 MW; 5566866E CRC32;
                                                                   |||||| || : | ||| || || || |||; :|
301 LAPVAEMALGEHGAAALGEVRAALDAAATKLGLSL 335
                                                  297 LAPVAARALQDAGRAALDEVREQFHARAARLGIAL 331
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Best Local Similarity 62.9%
Matches 207; Conservative
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                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        degradation.";
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Q52570;
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PRELIMINARY;
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Q52162;
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239 VRACGTGLAVVTEFMNDWRDEHVRWVDAVVQTAAAESEANRALLSRWAGEARAQAAEALR 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 931298//.
. SIE C.C., POH C.L.;
and sequences of the first eight genes of the chromosomally (methyl) phenol degradation pathway from Pseudomonas putida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: PHENOL + NADPH + O(2) = CATECHOL + NADP(+) +
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-!- COFACTOR: FAD FLAVOPROTEIN, AND REQUIRES FE(+2) FOR ACTIVITY (BY
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EMBL; X79063; CAA55661.1; -.
                                                                                                                     LDVLVPLRHAAWGANMNNAQICALGYGTVFTAPAMFHAMDNLGVAQYLTRLALAM--AEP
                                                                         120 TDGLLPLRHVEWAANMNNFYCADYGWGTAITQACTYCAMDRLGIAQYLSRIGLLLDGNTG
                                                                                                       179 DVLEAAKATWIRDAAWQPLRRYVEDILVVADPVELFIAQNLALDGLLYPLVYDRFVDERI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
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-!- FUNCTION: CATABOLIZES PHENOL, AND SOME OF ITS METHYLATED
DERIVATIVES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 331;
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11998 (TrEMBLrel. 06, Last sequence update)
1998 (TrEMBLrel. 08, Last annotation update)
HYDROXYLASE PI PROTEIN (EC 1.14.13.7)
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46.8%; Pred. No. 1.3e-56;
tive 54; Mismatches 115;
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Best Local Similarity 46.88
Matches 155; Conservative
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STRAIN-P35X / NCBI 9869;
MEDLINE; 95129877.
                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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SEQUENCE 331 AA; 381
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01-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- CATALYTIC ACTIVITY: PHENOL + NADPH + O(2) = CATECHOL + NADP(+) +
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-i- SUBUNIT: THE MULTICOMPONENT ENZYME PHENOL HYDROXYLASE IS FORMED PO, P1, P2, P3, P4 AND P5 POLYPEPTIDES.
EMBL; X80765; CAA56741.1; -.
DVLEAAKATWTRDAAWQPLRRYVEDTLVVADPVELFIAQNLALDGLLYPLVYDRFVDERI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aromatic hydrocarbons catabolism; Oxidoreductase; Monooxygenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid pPCH1.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 95272534.
HERRMANN H., MUELLER C., SCHMIDT I., MAHNKE J., PETRUSCHKA L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOI. Gen. Genet. 247:240-246(1995).
-1- FUNCTION: CATABOLIZES PHENOL, AND SOME OF ITS METHYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Localization and organization of phenol degradation genes Pseudomonas putida strain \mbox{H.}^{"}\mbox{;}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
11-JUN-1998 (TrEMBLrel. 08, Last annotation update)
PHENOL HYDROXYLASE PI PROTEIN (EC 1.14.13.7)
(PHENOL 2-MONOOXYGENASE PI COMPONENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.7%; Score 770.5; DB 2;
46.5%; Pred. No. 6.1e-56;
:ive 54; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     430445B9 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                          342
                                                                                                                                                                                                                                                 PVAARALQDAGRAALDEVREQFHARAARLGI 329
                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Flavoprotein; FAD; Iron; Plasmid
SEQUENCE 342 AA; 39370 MW; 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 46.5%
Matches 154; Conservative
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Length 333;

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299 310

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121 LDVLVPLRHAAWGANMNNAQICALGYGTVFTAPAMFHAMDNLGVAQYLTRLALAM--AEP 178
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MEDLINE; 98432776.
MEDLINE; 98432776.
BERTOIN G., MARTINO M., GALLI E., BARBIERI P.;
"Analysis of the gene cluster encoding toluene/o-xylene monooxygenase from Pseudomonas stutzeri OX1.";
from Pseudomonas stutzeri OX1.";
                                                                                                                                                                                                                                                                                                                                          61 PSRSAIRMANWYALKDPRQFYYASWATTRARQQDAMESNFEFVESRRMIGLMRDDVAARA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 ALEGGSAVAMLTAFMPEWHTESNRWIDAVVKTMAAESDDNRALLARWTRDWSARAEAALA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MIIELKTVDIKPLRHTFAHVAQNIGGDKTATRYQEGMMGAQPQENFHYRPTWDPDYEIFD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 DVLEAAKATWTRDAAWQPLRRYVEDTLVVADPVELFIAQNLALDGLLYPLVYDRFVDERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas stutzeri (Pseudomonas perfectomarina).
Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
                                                  HORIMOCHI M., KASUGA K., NOJIRI H., YAMANE H., OMORI T., "Cloning and characterization of genes encoding an enzyme oxidizes dimethyl sulfide in Acinetobacter sp. strain 208. FEMS Microbiol. Lett. 155:99-105(1997).
EMBL; D85089; BAAZ3331.1; -. SEQUENCE 333 AA; 38393 MW; BC106309 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IKPLRHTFAHVAQNIGGDKTATRYQEGMMGAQPQENFHY ----RP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-NOV-1998 (TrEMBLrel. 08, Last annotation update) TOLUENE, O-XYLENE MONOOXYGENASE OXYGENASE SUBUNIT.
                                                                                                                                                                                               37.2%; Score 640.5; DB 2;
38.7%; Pred. No. 3e-45;
1ive 69; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.9%; Score 222.5; DB 2; 25.1%; Pred. No. 8.2e-11; tive 52; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4EFF1AD8 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                                                                                                                    Conservative
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Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
   FROM N.A
                                     MEDLINE; 98005684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas.
                                                                                                                                                                                                                                    Matches 129;
                    STRAIN-20B;
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Best Local S
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   309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDVLVPLRHAAWGANMNNAQICALGYGTVFTAPAMFHAMDNLGVAQYLTRLALAM--AEP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 ALEGGSAVAMITAFMPEWHTESNRWIDAVVKTMAAESDDNRALLARWTRDWSARAEAALA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIIELKIVDIKPLRHTFAHVAQNIGGDK TATRYQEGMMGAQPQENFHYRPTWDPDYEIFD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 TENGGSDVAMLTEFMRDWYGESTRWVDAMFKTVLAENDANREQVQAWLEVWEPRAYEALL
                                                                                                                                                                                                                                                                                                                                                                                                                          expression of genes encoding phenol hydroxylase and catechol 1,2-dloxygenase in Acinetobacter calcoaceticus NCIB8250.";
Mol. Microbiol. 18:13-20(1995).

EMBL, 236909; CAA85381.1; -
SEQUENCE 333 AA; 38382 MW; 83055EC9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVLEAAKATWTRDAAWQPLRRYVEDTLWADPVELFIAQNLALDGLLYPLVYDRFVDERI
                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
Moraxellaceae; Acinetobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                 of
                                                                                                                                                                                                                                                                                                                                                                                          EHRT S., SCHIRMER F., HILLEN W.; "Genetic organization, nucleotide sequence and regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                              01, Last sequence update)
08, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 640.5; DB 2;
; Pred No. 3e-45;
70; Mismatches 120;
                                                                                                                                                             333 AA
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                                   PVAARALQDAGRAALDEVREQFHARAARLGI 329
                                                     Crėated)
                                                                                                                                                                                                 Created
                                                                                                                                                             PRT;
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Bacteria; Proteobacteria; gamma
Moraxellaceae; Acinetobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 AWAQTALTDSGIDSGLNKISER 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.2%;
39.4%;
                                                                                                                                                                                                 01,
                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1998 (TrEMBLrel. 08, PHENOLHYDROXYLASE COMPONENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLEEL. 05, 01-JAN-1998 (TrEMBLEEL. 05, 01-NOV-1998 (TrEMBLEEL. 08, DMS OXYGENASE COMPONENT.
                                                                                                                                                                                                                                                                    Acinetobacter calcoaceticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 37.2%
Best Local Similarity 39.4%
Matches 127; Conservative
                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01-NOV-1996 (TrEMBLrel.
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MEDLINE; 96154937
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Q43979;
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STRAIN-JMP134;
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01-NOV-1996
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01-AUG-1998
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Matches 8
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                        RESULT 11
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                                                                                                                                       | | | | | | | | | | | ADSL---RWLTHTAYRIKELSQIFSDLGFGIDERRYWEQDPAWQGWRKLVEHALVAWDWA 215
PDYEIFDPSRSAIRMANWYALKDPRQFYYASWATTRARQQDAMESNFEFVESRRMIGLMR 113
            ----LAMAEPDV--LEAAKATWTRDAAWQPLRRYVEDTLVVADPVELFIAQNLALDGLLY 226
                                                                                                                          PLVYDRFVDERIAL --- EGGSAVAMLTAFMPEWHTESNRWIDAVVKTWAAESDDNRALLA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 MDNLGVAQYLTRLALAMAEPDVLEA-----AKATWTRDAAWQPLRRYVEDTLVVADPV 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELFIAQNLALDGLLYPLVYD---RFVDERIALEGGSAVAMLTAFMPEWHTESNRWIDAVV 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EI---FDPSRSA--IRMANWYALKDPRQFYYASWATTRARQQDAMESNFEFVESRRMIGL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112, MRDDVAARALDVLV------PLRHAAWGANMNNAQICALGYGTVFTAPAMFHA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|||:|::|:|
8 LKPLK-TWSHLA------ARR------RRPSEXEIVSTNLHYTTDNPDAPFELDPNF 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KTMAAESDDNRALLARWTRDWSARAEAALAPVAARALQDAGRA---ALDEVREQFHA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 DDVAARALDVLVPLRHAAWGANMNNAQICALGYGTVFTAPAMFHAMDNLGVAQYLTRLA-
                                                                                                                                                                                                                                                                                                                Burkholderia pickettii (Pseudomonas pickettii).
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82;
                                                                                                                                                                                                                                                                                                                                                                            MEDILNE; 95172404.
BYRNE A.M., KUKOR J.J., OLSEN R.H.;
"Sequence analysis of the gene cluster encoding toluene-3-monooxygenase from Pseudomonas pickettii PKOl.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.2%; Score 193; DB 2; Length 32 24.6%; Pred. No. 2.2e-08; tive 55; Mismatches 132; Indels
                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1998 (TrEMBLrel. 08, Last annotation update) TOLUENE-3-MONOOXYGENASE OXYGENASE SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       329 AA; 37525 MW; C61B3727 CRC32;
                                                                                                                                                                                                                                          329 AA.
                                                                                                                                                                               RWTRDWSARAEAALAPVAARALQDAGRAALD 314
                                                                                                                                                                                                                                                               01, Created)
                                                                                                                                                                                                                                          PRT;
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EMBL; U04052; AAB09622.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L Similarity 24.6
88; Conservative
                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel).
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Monooxygenase.
SEQUENCE 329
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01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                      STRAIN-PRO1
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Best Local 8
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Q51943;
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Q51943
                                                                                173
                                                                                                                                                                  284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MRDDVAARALDVLVPLRHAAWGANMNNAQICALGYGTVFTAPAMFHAMDNLGVAQYLTRL 1171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 AYRTRELSQIFGDVGFGTDERRYWEQDPAWQGWRKLVEHALVAWDWAECFVAFSLVLRPA 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 IKPLRHTFAHVAQNIGGDKTATRYQEGMMGAQPQE-----NFHYRP-----TWDPDY 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                             Alcaligenes eutrophus.
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 332;
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Erment. Bloong. 799-406(1994).

EMBL; D37875; BAA07112.1; -.

SEQUENCE 343 AA; 38462 MW; 9195C333 CRC32;
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Actinomycetales; Corynebacterineae; Nocardiaceae; Nocardia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HARKER A.R., AYOUBI P.J.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF065891; AAC77384.1; -.
SEQUENCE 332 AA; 37511 MW; 871144CB CRC32;
                                                                                                      (TrEMBLrel. 07, Created)
(TrEMBLrel. 07, Last sequence update)
(TrEMBLrel. 07, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.1%; Score 190.5; DB 2 25.1%; Pred. No. 3.6e-08; tive 53; Mismatches 145
     Ä
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332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                            PUTATIVE HYDROXYLASE COMPONENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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HLA-RLLHVEGDELDSLV---LRNLHGDAQRHARWTAALGRFAVEQNVNNRTVLRDAIAG 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 VLDPRWAGKLARLYTPARYLFHTLQMASAYVGTDGSLQATITNCQLLSDGLNPFRWWSHT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 AIPAVEEAVLRKIGESGQHNGDTLVGLLNDAQLVDAARHRRWAATLVKMAVEKAGQRRTL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 MWMNRWYKQNTLNSPLKHDDWNAFRDPDQVIYRTYNLMQDGQEAYVYGLFDQFNAREHDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 IMRDDVAARALDVLVPLRHAAWGANMNNAQICALG--YGTVFTAPAMFHAMDNL---GVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 AYRTKELSLAFDDKSFGTDERQYWETDPAWGGFRELMEKVLVTWDWAEAFVAFSL----V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 QYLTR-LALAMAEPDVLEAAKATWTRDAAWQPLRRYVEDTLVVADPVELFIAQNLALDGL
                                                                                                                                                                                                                                                                 Burkholderia cepacia (Pseudomonas cepacia).
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methylocystis sp. M.
Bacteria; Proteobacteria; alpha subdivision; Methylocystaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.8%; Score 134; DB 2; Length 33 21.2%; Pred. No. 0.0016; Live 55; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                STRAIN=AA1;
MA Y., HERSON D.S.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF001356; AABS8744.1; -.
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-01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
-01-NUV-1998 (TrEMBLrel. 08, Last annotation update)
SOLUBLE METHANE MONOOXYGENASE PROTEIN A BETA SUBUNIT.
                                                                                                                                                                                                Last sequence update)
Last annotation update)
                              289 WSARAEAALAP----VAARA-LQDAGRAALDEVR---EQFHARA
                                                   286 IKKMGSSKWEPLADSAITAYCTALSDVPDASASARLATRE 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282 LARW-TRDWSARAEAALAP--VAARALQDAGRAALDEVRE 318
                                                                                                                                                                                                                                                                                                                                                                                                                                 332 AA; 38195 MW; B7C79FC3 CRC32;
                                                                                                                                                 332 AA
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                                                                                                                                                                                  Created)
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Best Local Similarity 21.2%
Matches 72; Conservative
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SEQUENCE 337
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01-AUG-1998
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                                                                                                                                                                                            83 LWQRPYVSTCNQDQQAL...-ARLVPVLIMGSAA----ITPIWSQKILARSYAA 128
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                                                                                                                                                                                                                                                                                                                 SAVAMLTAFMPE - - WHTESNRWIDAVVKTMAAE - - - SDDNRALLARWTRDWSARAEAA - - 296
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                                                               Gaps
                                                                                                                                                            80 FYYASWATTRARQODAMESNFEFVESRRMIGLMRDDVAARALDVLVPL------RHAA 131
                                                                                                                                                                                                                               W-----GANMNNAQICALGYGTVFTAPAMFHAMDNLGVAQYLT-RLALAMAEPDVLEA-A 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 AMAEP--DVLEAAKATWTRDAAWQP,LRRYVEDTLVVADPVELFIAQNLALDGLLYPLVYD 231
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                                                                                           31 TRYQEGMMGAQ--PQENFHY-----RPTWDPDYEIFDPSRSAIRMANWYALKDPRQ 79
                                                                                                                 STRAIN-PY2;
ZHOU N.Y., CHAN KWO CHION C.K., LEAK D.J.;
ZHOU N.Y., CHAN KWO CHION C.K., LEAK D.J.;
The alkene monooxygenase from Xanthobacter Py2 is closely related aromatic monooxygenase and catalyses aromatic monohydroxylation of benzene, toluene and phenol.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ012090; CAA09915.1;
SEQUENCE 341 AA; 38223 MW; 8775471D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xanthobacter sp. Py2.
Bacteria; Proteobacteria; alpha subdivision; Ancylobacter group;
Xanthobacter.
                                                               59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37;
                              Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 341;
                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence update)
annotation update)
                             Score 179.5; DB 2;
Pred. No. 3e-07;
55; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 9.7%; Score 167.5; DB 2; Best Local Similarity 26.1%; Pred. No. 2.9e-06; Matches 74; Conservative 49; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                               297 -LAPVAARALQDAGRAALDEVREQFHARAARLGIAL 331
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                             10.4%; 22.9%;
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                                                             Conservative
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                                              Similarity
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                              Query Match
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           MCDONNLD I.R., DCHIYAMA H., KAMBE S., YAGI O., MURRELL J.C.;
"The soluble methane monooxygenase gene cluster of the
trichloroethylene-degrading methanotroph Methylocystis sp. strain M.";
Appl. Environ. Microbiol. 63:1898-1904(1997).
EMBL: U81554; AAC45290.1; -.
MONOOXygenase.
SEQUENCE 395 AA; 45170 MW; E4507FBD CRC32;
                                                                                                                                                                                                                                                                                                                                                                          184 AKATWIRDAAWQPLRRYVEDTLV-VADPVELFIAQNLALDGLLYPLVYDRFVDERIALEG 242
                                                                                                                                                                                                                                                                                       73 ALKDPRQFYYASWA---TTRARQQDAMESNFEFVESRRMIG-LMRDDVAARALDVLVPLR 128
                                                                                                                                                                                                                                                                                                           129 HAAWGANMNNAQICALGYGTVFTAPAMFHAMDNLGVAQ--YLTRLALAMAEPDV---LEA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 GSAVAMLTAFMPEWHTESNRWIDAVVKTMAAESDD----NRALLARWTRDWSARAEAAL- 297
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                         28 KTATRYQEGMMGAQPQ------ENFH-YRPTWDPDYEIFDPSRSAIRMANWY 72
                                                                                                                                                         Query Match 7.1%; Score 121.5; DB 2; Length 395; Best Local Similarity 20.8%; Pred. No. 0.022; Matches 68; Conservative 50; Mismatches 164; Indels 45;
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Search completed: September 26, 2000, 20:28:52 Job time: 1011 sec The second

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 26, 2000, 20:22:37; Search time 60.65 Seconds (without alignments)

22.495 Million cell updates/sec

Title: US-09-430-029-4

Perfect score: 451
Sequence: 1 MSNVFIAFQANEDSRPIVDA.....ITLSGHIDEDDDEFTLSWSH 89

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 152396 seqs, 15329161 residues

Total number of hits satisfying chosen parameters: 152396
```

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/cCOMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 10, Appl	Sequence 5, Appli	Sequence 3, Appli	Sequence 32, Appl		Sequence 78, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 15, Appl	Sequence 6, Appli	Sequence 6, Appli	Ġ.	
US-08-105-454-10	US-08-766-858A-5	US-08-387-942C-3	US-08-576-626A-32	US-08-484-905-78	US-08-481-985B-78	US-08-597-236-2	US-08-746-682A-2	US-08-049-254-2	US-08-472-934-2	US-08-323-460A-2	US-08-461-146C-2	US-08-461-145C-2	US-08-487-031-15	US-08-451-946B-6	US-08-446-938B-6	US-08-446-939B-6	
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55.5	55.5	55.5	55.5	55	55	52	52	52	52	55	52	55	54	54	54	54	
29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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GS-08-319-387-3

| Sequence 3. Application US/08319387
| Sequence 3. Application US/08319387
| Patent No. 5543137
| GENERAL INFORMATION:
| APPLICAWT: Francesconi Stephen C. |
| TITLE OF INVENTION: Microbial Degradation of Trichloroethylene, TITLE OF INVENTION: Microbial Degradation of Trichloroethylene, TITLE OF INVENTION: Microbial Degradation of Trichloroethylene, TITLE OF INVENTION: Microbial Degradation of Trichloroethylene, TITLE OF INVENTION: Microbial Degradation of Trichloroethylene, TITLE OF INVENTION: Microbial Defrace Addresses: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1
| CITY: Gainesville STREET: 2566 |
| COMPUTER READABLE FORM: MEDICAL N.W. 41st Street, Suite A-1
| STREET: 3266 |
| COMPUTER READABLE FORM: MADINE FOLDS/MS-DOS SOFTWARE: PRICAMIN STREET PROPOSEMENT OF DOS/MS-DOS SOFTWARE: PRICAMIN NAMER: US/08/319,387 |
| FILING DAME: DEC-1993 |
| CLASSIFICATION NUMBER: US 07/694,718 |
| FILING DAME: 02-MAY-1991 |
| CLASSIFICATION NUMBER: US 07/694,718 |
| FILING DAME: Whitlock, Ted W. |
| APPLICATION NUMBER: US 07/694,718 |
| FILING DAME: Whitlock, Ted W. |
| RESISTRATION FOR EQUID ON 3 |
| SEQUENCE CHARACTERISTICS: |
| ELEBHONE: 904-375-8100 |
| TELECOMMUNICATION INVESTIGES |
| TELECOMMUNICATION INVESTIGES |
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| TYPE: Mallo OF STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STR
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                                                                                                                                                                                                                                                                         DB 2; Length 1162;
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                                                                                                                                                                                                                                                                       14.4%; Score 65; DB 2; Length 116
26.7%; Pred. No. 6.7;
ive 11; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Application US/08023610
Patent No. 5928648
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D, Mark D
APPLICANT: Macdonald Ph.D., Alchard D
TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys
TITLE OF INVENTION: and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                      49 RETIEEL-TGTRFDLQQLQVNLITLSGHIDEDD----DEFTLSWS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/023,610
FILING DATE: February 26, 1993
CLASSIFICATION: 435
TATORNEY/AGENT INFORMATION:
NAME: White Esg, John P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.4%; Score 65; DB; 26.7%; Pred. No. 6.7; tive 11; Mismatches
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MEDIUM TYPE: Floppy disk
CMDMTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
    TELECOMMUNICATION INFORMATION:
                                                             TELEX: 422523
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1162 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212)977-9550
TELERAX: (212)664-0525
TELEX: 42253
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1162 amino acids
                                                                                                                                                                                                                                                                                                                                                        4 VFIAFQANEDSRPIVDAIVA---
                     TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
                                                                                                                                                                                                                                                                       Query Match 14.4%
Best Local Similarity 26.7%
Matches 28; Conservative
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Best Local Similarity 26.78
Matches 28; Conservative
                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-663-566A-15
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CORRESPONDENCE ADDRESS:
                                                                                                                                                    amino acid
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New York
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US-08-023-610-15
                                              TELEFAX:
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                                            Gaps
                                                                                1 MSNVFIAFQANEDSRPIVDAIVADNPRAVVVĖSPGMVKIDAPDRLTIRRETIEELTGTRF 60
                                                                                                        2 SNVFIAFQANEDSRPIVDAIVADNP-RAVVVES-PGMVKIDAPDRLTIRRETIEELTGTR 59
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                                                                                                                                                                                                                                                                                                                          APPLICANT: YEN, KWANG-MU; BLATT, LAWRENCE M.; KARL, MICHAEL R.; TITLE OF INVENTION: BIOCONVERSIONS CATALYZED BY THE TOULUENE; MONOOXYGENASE OF PSEUDOMANAS MENDOCINA KR-1
NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 103;
78.7%; Score 355; DB 1; Length 92; 73.0%; Pred. No. 1.8e-39;
                                        Indels
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APPLICANT: Cochran, Mark D
APPLICANT: Macdonald, Richard D
TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys
TITLE OF INVENTION: and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,566A
FTI.NG DATE: June 13, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 122; DB 5;
; Pred No. 7.4e-09;
21; Mismatches 33
                                        14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/590,374
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 177,631
FILING DATE: 05-APR-1988
                                                                                                                                                                 61 DLQQLQVNLITLSGHIDEDDDEFTLSWSH
                                                                                                                                                                                        63 DLQQIHINLITLSGYIDEDDEQFTLSWKH
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US-08-663-56A-15
Sequence 15, Application US/08663566A
; Patent No. 5853733
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72 FNMQELEINLASFAGQIQADEDQ 94
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REGISTRATION NUMBER: 28,678
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32.58;
                                          Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 27; Conserv
                     Best Local Similarity
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5171684-5
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  Query Match
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934 VFIHFSYTPDSFVNVTAIVGFCVKPANASQYAIVPANGRGIFIQVNGSYYITARDMYMPR 993
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APPLICANT: Cochran, Mark D
APPLICANT: Junker, David
APPLICANT: Wild, Martha A
TITLE OF INVENTION: Recombinant Herpesvirus and Uses Thereof
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 1162;
                                                                                                                                                                                                                                                        APPLICANT: Cochran, Mark D
APPLICANT: Cochran, Mark D
APPLICANT: Macdonald, Richard D
TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys S-
TITLE OF INVENTION: Necombinant Herpesvirus of Turkeys S-
TITLE OF INVENTION: 4PT-050 and Uses Thereof
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Mismatches 46; Indels
                                                                        994 AITAGDIVTLTSCQANYVSVNKTVITTFVDNDDFDFNDELSKWWN 1038
                                          49 RETIEEL-TGTRFDLQQLQVNLITLSGHIDEDD----DEFTLSWS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 RETIEEL-TGTRFDLQQLQVNLITLSGHIDEDD----DEFTLSWS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 6.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.4%; Score 65; 26.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/288,065A FILING DATE: Aug-09-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                           Sequence 15, Application US/08288065A Patent No. 5961982 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15, Application US/08362240A
Patent No. 5965138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)391-0526
TELEFAX: (212)391-0526
TELEFAX: 422523
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1162 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 26.75
Matches 28; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      435
                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
STATE: New York
COUNTRY: USA
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Sequence 15, Application PC/TUS9510245
GENERAL INFORMATION:
APPLICANT: SYMTRO CORPORATION
TILLE OF INVENTION: Recombinant Herpesvirus of Turkeys And Uses Thereof
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               934 VFIHFSYTPDSFVNVTALVGFCVKPANASQYALVPANGRGIFLQVNGSYXITARDMYMPR 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 VFIAFQANEDSRPIVDAIVA------DINPRAVVVESPGMVKIDAPDRLTIR, 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,240A
FILING DATE: Dec-22-94
CLASSIFICIAN: 435
ATTORNEY/Accurr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 RETIEEL-TGTRFDLQQLQVNLITLSGHIDEDD----DEFTLSWS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.4%; Score 65; DB 26.7%; Pred. No. 6.7; tive 11; Mismatches
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: John P. White STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, V¢ CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/10245 FILING DATE: 09-AUG-1995
                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)378-0400
TELEFAX: (212)391-0526
                                                                                                                                                                                                                                                                                                                                            28,678
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TELEPHONE: (212)278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 422523
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1162 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Las 28; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New York
                                          New York
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                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-362-240A-15
                                                            COUNTRY:
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TRANSGENIC PLANTS INCLUDING A HYBRID NUCLEIC ACID SEQUENCE, COMPRISING AN UNEDITED MITOCHONDRIAL GENE FRAGMENT FROM HIGHER PLANTS AND PROCESS FOR PRODUCING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 DSRPIVDAIVADNPRAVVVESPGMVKIDAPDRLTIRRETIEELTGTRFDLQQLQVNLITL 72
                                                             ------SMLAI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 DAIVADNPR-AVVVESP-GMVKIDAPDRLTIRRETIEELTGTRFDLQQLQVNLITLSGHI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 406;
                                                                                                                                                                                                                                                  ; APPLICANT: DEAN, CAROLINE; HARDER, PATRICIA A.; LETO, KENNI; J.O. KEERE, DANIEL P.; OWER; A.; ROMESSER, JAMES A.; TEPPERAKN, JAMES M.; TIPPERRAKN, JAMES M. TITLE OF INVENTION: EXPRESSION OF HERBICIDE METABOLIZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 62.5; D
Pred. No. 3.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Mismatches
                                                                                                                                                                                                                                                                                                                 CYTOCHROMES

NUMBER OF SEQUENCES: 19

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/569,781

FILLING DATE: 23-AUG-1990

PRIOR APPLICATION NUMBER: 464,499

FILLING DATE: 12-JAN-1990

APPLICATION NUMBER: 465,605

FILLING DATE: 11-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/505,218 FILING DATE: 03-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                             20 DSRPSSPALYFTHDASLVHKSP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: RRATA, ALEJANDRO
APPLICANT: MOURAS, ARWAND
TITLE OF INVENTION: UNCLEIC ACII
TITLE OF INVENTION: MUCLEIC ACII
TITLE OF INVENTION: MITOCHONDRIT
TITLE OF INVENTION: POR PRODUCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08505218 Patent No. 591447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.9%;
Best Local Similarity 35.5%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                        |||:| |||
62 SGHLDSDDD 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                              73 SCHIDEDDD
                                                                                                                                                                                         RESULT 9
5212296-6
;Patent No. 5212296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 406
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US-08-505-218-6
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CITY: Al
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                                                                                                                                                                                                                                                                        --- DNPRAVVVESPGMVKIDAPDRLTIR 48
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                                                                                                                                                                         DB 4; Length 1162;
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pred. No. 1.3;
Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                     994 AITAGDIVTLISCQANYVSVNKTVITTFVDNDDFDFNDELSKWWN 1038
                                                                                                                                                                                                                                                                                                                         49 RETIEEL-TGTRFDLQQLQVNLITLSGHIDEDD----DEFTLSWS 88
                                                                                                                                                                                                             46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: HUMAN TSC-22-LIKE PROTEIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER REACABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                       Score 65; DB 4
Pred. No. 6.7;
                                                                                                                                                                                                             11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF-0285 US
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FILING DATE: Herewith
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08851190 Patent No. 6074843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE, DOCKET NUMBER: PE-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13
                                                                                                                                                                                                                                              4 VFIAFQANEDSRPIVDAIVA----
                                                                                                                                                                       14.48;
26.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 292 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.28; 24.68;
                                       1162 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UMBER:
FILING DATE:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                           28; Conservative
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Matches 17; Conservative
                     SEQUENCE CHARACTERISTICS
                                                                                          ; MOLECULE TYPE: protein PCT-US95-10245-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                       EQUENCTH: 1162 cm.
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: TONSNOT01
CLONE: 736663
                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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-17

5

Gaps

46;

31; Indels

Length 897;

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58 NVTLIRRVNEDLLEPVSCDLSDDMPWSACPHPRCVPRRCVIPCQSFVVTDVDYFSFQPDR 117
                                                                                                                                                                                                                                                                           3 NVFIAFQANEDSRPIVDAIVADN-----PRAVVVESPGMVKIDA-----PDR 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --GMVKIDAPDRLTIRRETIEELTGTRFDLQQLQVNLITL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 -----PLGTRL-----TVTLTQHVQPPEPRDLQISTDQDHFLLTWS 153
; OTHER INFORMATION: Human GM-CSF receptor; Signal Sequence: US-07-960-389-2
                                                                                                                                                                                                                                                                                                                                                                                                        45 LTIRRETIEELTGTRFDLQQLQVNLITLSGH-------IDEDDDEFTLSWS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Stiegler, Gary
APPLICANT: Silver, Gary
APPLICANT: Silver, Gary
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES AND USES THEREOF
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.5%; Score 61; DB 3; Length 256; 22.9%; Pred. No. 2.6; tive 16; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PELLIANG DATE:
FILING DATE:
                                                                                                                                                 DB 1;
                                                                                                                                                                                                       9; Mismatches
                                                                                                                                              Score 62; DB
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 89, Application US/08906769
Patent No. 6077687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 89:
                                                                                                                                       Query Match 13.7%;
Best Local Similarity 24.6%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (303) 863-9700
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 NPRAVVVESP-----
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Colorado
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-08-906-769-89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 13.7%; Score 62; DB 2; Length 322; Best Local Similarity 32.1%; Pred. No. 2.7; Matches 27; Conservative 12; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: HAYASHIDA, Kasuhiro;
TITLE OF INVENTION: Human GM-CSF Receptor Component
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: System Software 7.1 SOFTWARE: Microsoft Word 5.1a CURRENT APPLICATION DATA: CLASSIFICATION NUMBER: US/07/960,389 FILING DATE: 07-JAN-1993 CLASSIFICATION 800 PRIOR APPLICATION NUMBER: 554,745 FILING DATE: 18-JUL-1990 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 05-JUL-1991 APPLICATION NUMBER: 
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STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
                                                                                                        1169-013
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REGISTRATION NUMBER: 31,895
REFERENCE/DOCKET NUMBER: DX0143Q
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             288 EIRGINHAFIPIVVEAVILKDYAD 311
                                     NAME: KRAUS, ERIC J
REGIESTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 1169
TELECOMMUNICATION INFORMATION:
TELEPRONE: (703) 684-1111
TELEPRAX: (703) 684-1124
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 322 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/07960389
Patent No. 5705611
GENERAL INFORMATION:
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TELEFAX: (908) 298-5388
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 897 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disc
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 8
          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-505-218-6
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STRANDEDNESS: sir
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US-08-74-725-22

Sequence 22, Application US/08748725

Patent No. 5859346

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street
                            GENERAL INFORMATION:
APPLICANT: Zhang et al.
TITLE OF INVENTION: CRUCIFER AFT PROTEINS AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ESPGMVKIDAPDRLTI--
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                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/266,451B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTY CONTY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 23-June-1994
CLASSIFCATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/219001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219 VHQTASLGDVEGLKAALAS-GGNKDEEDSE 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 25.6'
Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts COUNTRY: U.S.A.
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STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY:
US-08-266-451B-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Arfsten, Ann
APPLICANT: Dale, Beverly
APPLICANT: Stiegler, Gary
TITLE OF INVENTION: USE OF PROTEASE INHIBITORS AND
TITLE OF INVENTION: PROTEASE VACCINES TO PROTECT ANIMALS FROM FLEA
TITLE OF INVENTION: INPESTATION, AND FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ij
90 HPXAQIIKHPAYGNVTDIDMEXALIKVRRPFRLNNRTVRTVKLTDVGKDMPSGELATVTG 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .0, Version #1.25
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22.9%; Pred. No. 2.6;
tive 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #110, Ve. CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14442A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                                             Sequence 89, Application PC/TUS9514442k
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hunter, Shirley Wu
APPLICANT: Frank, Glenn R.
APPLICANT: Heath, Andrew W.
APPLICANT: Yamaka, Miles Yamanaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22, Application US/08266451B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Gary J. Connell
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEFAX: (303) 863-9700
TELEFAX: (303) 863-023
INFORMATION FOR SEQ ID NO: 89:
                                                                                                                                                                                                                                                                                                                                                                                 Grieve, Robert B. Rushlow, Keith E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 256 amino acids TYPE: amino acid
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Best Local Similarity 22.9%
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
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                                                                                                           |::||:|
| 150 WGNLGEDEDD 159
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| 150 WGNLGEDEDD 159
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STATE: Colorado
COUNTRY: USA
                                                                    73 SCHIDEDDDE 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 SGHIDEDDDE 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                            PCT-US95-14442A-89
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US-08-266-451B-22
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                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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Search completed: September 26, 2000, 20:22:40 Job time: 3814 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

September 26, 2000, 20:24:12; Search time 82.1 Seconds (without alignments) 67.086 Million cell updates/sec Run on:

US-09-430-029-4
451
1 MSNVFIAFQANEDSRPIVDA.....ITLSGHIDEDDDEFTLSWSH 89 Title: Perfect score: Sequence:

Scoring table:

178050 segs, 61884766 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

178050 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_64:* Database :

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result No.	Score	Query Match	gth	DB	ID	Description
1	247	54.8		-	S44305	phenol 2-monooxyge
7	247	54.8	90	П	C37831	
m	232	51.4		٦	S47289	
4	83.5	18.5		7	T36380	٦
S	77	17.1	1684	7	T02632	hypothetical prote
9	70.5	15.6	174	N	G69411	small heat shock p
7	69	15.3	822	7	S77112	DNA mismatch repai
80	68.5	15.2	143	7	D75617	response requlator
თ	67.5	15.0	410	7	JC4287	cytochrome P450 sc
10	66.5	14.7	2277	7	B47648	perlecan homolog u
11	66.5	14.7	2295	~	T19820	hypothetical prote
12	66.5	14.7	2482	7	T19819	
13	66.5	14.7	2482	7	A47648	0
14	66.5	14.7	3375	7	T19821	hypothetical prote
12	99	14.6	138	N	D39049	methane monooxygen
16	99	•	181	7	A40607	monofunctional cho
17	99	14.6	294	7	D81430	UDP-3-0-[3-hydroxy
18	99	14.6	390	7	C69276	coenzyme F420qui
19	99	14.6	619	7	A43361	Ets-related transc
20	99	14.6	649	7	S74823	N-acetylmuramoyl-L
21	65	14.4	1162	7	S07421	E2 glycoprotein pr
22	65		1232	7	S40766	hypothetical prote
23	64.5	14.3	316	7	B47157	magnesium transpor
24	64.5		452	~	I49595	cytokeratin 15 - m
25	64	14.2	347	7	A75537	hypothetical prote
56	64	14.2	487	Н	BWSOGM	gtfA protein - Str
27	64	14.2	1162	7	S14939	E2 glycoprotein pr
28	63.5	14.1	224	7	m	transcription regu
29	63.5	14.1	394	N	T06180	methionine adenosy

RESULT 2 C37831 phenol 2-monooxygenase (EC 1.14.13.7) chain P2 - Pseudomonas sp. (strain CF600) C;Species: Pseudomonas sp.

-	diaminopimelate de	methionine adenosy	extracellular prot	probable membrane	riboflavin synthas	late competence op	methionine adenosy	cytochrome P450 10	hypothetical prote	pipecolate-incorpo	hypothetical prote	dexA.1 protein - p	histocompatibility	cytochrome-c oxida	cytochrome-c oxida	cytochrome-c oxida
	DCECD	S66351	S21596	S56250	A69052	S39863	T06592	A35401	T21865	T30227	T17484	D32338	169005	OBWT2	S54306	T01704
	_	~	7	~	7	7	~	7	~	7	٣	7	N	-	~	7
	420	366	557	828	139	205	360	406	964	1541	4077	80	166	260	260	260
	14.1	14.0	14.0	14.0	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.7	13.7	13.7	13.7	13.7
	63.5	63	63	63	62.5	62.5	62.5	62.5	62.5	62.5	62.5	62	62	62	62	62
	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

1;

Gaps

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Fleischman, R.D.; Quadkenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
Nature 390, 364-370, 1997
A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch A; Reference number: A69250; MUID: 98049343
                                              A.Accession: T36380
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-862 <OLI>
A.Cross-references: EMBL:AL049628; PIDN:CAB40869.1; GSPDB:GN00070; SCOEDB:SCE94.20
A.Steprimental source: strain A3(2)
C.Genetics:
A.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G69411
small heat shock protein (hsp20-1) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Jun-1998
C;Accession: G69411
R;Klenk, H.P.; Clayton, R.A.; Ton, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.;
R;Klenk, H.P.; Clayton, S.A.; Ton, M. H. C.; Nelson, G. C. Gill, S. Kirkness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Typecies: Homo sapiens (man)
C; Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 05-Nov-1999
C; Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 05-Nov-1999
C; Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 05-Nov-1999
C; Date: 05-Mar-1999 #sequence 05-Mar-1999 #text_change 05-Nov-1999
R; Bemis, G; Rohlfing, T; Morris, M.
submitted to the EMBL Data Library, July 1998
A; Description: The sequence of Homo sapiens PAC clone DJ1186C01.
A; Reference number: 214682
A; Accession: T02634
A; Accession: T02634
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-1684 < DEM>A; Cross-references: EMBL:AC004991; NID:g3342751; PIDN:AAC27675.1; PID:g3342752
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 RAVVVESPGMVKIDAPDRLTIRRETIEELTGTRFDLQQLQVNLITLSGHIDEDDDEFTLS 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNVFIAFQANEDSRPIVDAIVADNPRAVVVESPG----MVKIDAPDRLTIRRETIEELTG 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: intron positions not resolved (incomplete sequence) Note: WUGSC:H_DJ1186C01.1
                                                                                                                                                                                                                                                                                                                                                                                                            27;
                                                                                                                                                                                                                                                                                                                                                        ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein DJ1186C01.1 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                     18.5%; Score 83.5; DB 28.6%; Pred. No. 0.85; iive 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.1%; Score 77; DB: 26.7%; Pred. No. 8.6; Live 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 TRFDLQQLQVNLITLSGHIDEDDDEFTLSW 87
                                                                                                                                                                                                                                                                                                                                                                                                               18; Conservative
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Best Local Similarity
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A; Note: intron pos
A; Note: WUGSC: H_DJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     615 LAH 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 WSH 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phenol 2-monooxygenase (EC 1.14.13.7) chain mopM - Acinetobacter calcoaceticus
M;Alternate names: phenol hydroxylase
C;Species: Acinetobacter calcoaceticus
C;Species: Acinetobacter calcoaceticus
C;Accession: 570082; 847289
R;Ehrt, S: Schirmer, F: Hillen, W.
Mol. Microbiol. 18, 13-20, 1995
A;Title: Genetic organization, nucleotide sequence and regulation of expression of genes
A;Reference number: S70080; MUID:96154937
A;Status: nucleic acid sequence not shown; translation not shown
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: C3780.
B:Nordlund, I.; Powlowski, J.; Shingler, V.
J. Bacteriol. 172, 6826-6833, 1990
A:Title: Complete nucleotide sequence and polypeptide analysis of multicomponent phenol A:Reference number: A37831; MUID:91072230
A;Accession: C37831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-89 <EH2>
A; Cross-references: EMBL:236909; NID g535279; PIDN:CAA85382.1; PID:g535282
A; Experimental source: strain NCIB8250
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1994
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable large ATP-binding protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T36380
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, April 1999
                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M60276; GB:M37764; NID:g151449; PIDN:AAA25941.1; PID:g151452 C;Superfamily: phenol 2-monooxygenase component M C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Keywords: aromatic hydrocarbon catabolism; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 232; DB 1;
Pred. No. 2.9e-17;
1; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.8%; Score 247; DB 1;
51.1%; Pred. No. 8.2e-19;
tive 21; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 LQQLQVNLITLSGHIDEDDDEFTLSWSH | 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 LOQLQVNLITLSGHIDEDDDEFTLSWS 88
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46.0%;
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Best Local Similarity
Matches 40; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                           A; Residues: 1-90 <NOR>
                                                                                                                                                                                                                                 A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
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Dod ,

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Gaps

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Length 143;

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A)Cross-references: GB.AE001862; GB.AE001825; NID:g6460468; PIDN:AAF12176.1; PID:g646
A)Experimental source: strain R1
C)Genetics:
A)Gene: DRA0204
A)Map position: 2
C)Superfamily: chemotaxis cheY protein; response regulator homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-410 <WAT>
A;Cross-references: DDBJ:D30815; NID:91072316; PIDN:BAA06492.1; PID:d1007063; PID:910
A;Accession: PC4085
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C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Jul-1999
C; Accession: B47648
R; Rogalski, T.M.; Williams, B.D.; Mullen, G.P.; Moerman, D.G.
Genes Dev. 7, 1471-1484, 1993
A; Title: Products of the unc-52 gene in Caenorhabditis elegans are homologous to the A; Reference number: A47648; MUID:93339574
A; Accession: B47648
A; Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytochrome P450 sca-2 - Streptomyces carbophilus
C;Species: Streptomyces carbophilus
C;Species: Streptomyces carbophilus
C;Bate: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 04-Mar-2000
C;Accession: JC4287; Pc4085
R;Watanabe, II; Nara, F.; Serizawa, N.
Gene 163, 81-85, 1995
A;Title: Cloning, characterization and expression of the gene encoding cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 DPRLSSDRLHADFPATSPRFKAFRQGSPAFIGMDPPEHGTRRRWIISEFTVKRIKGMRPD 129
                                                                                                                                                                                                                                                                                                                                                                     15 RPIVDAIVADNPRAVVVESPGMVKIDAPDRLTIRRETIEELTGTRF------DLQQL 65
                                                                                                                                                                                                                                                                                                                                                                                                      2 RAIEILLTEDNPADILLTEEAFEEADFPHRLHVARDGVEALTFLRREENGELFTPDVILL 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Superfamily: Bacillus cytochrome P450 CYP106; cytochrome P450 homology Kseywords: chromoprotein; heme; iron; metalloprotein F; 245-381/Domain: cytochrome P450 homology e45> F; 359/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                               DB 2;
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                                                                                                                                                                                                                                                            15.2%; Score 68.5; Di 29.0%; Pred. No. 3.8;
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                                                                                                                                                                                                                                                                                                                   11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: JC4287; MUID:96001248
A;Accession: JC4287
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                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 2-9;11-21 <WA2>
C;Genetics:
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Best Local Similarity
        A; Residues: 1-143 <WHI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 QVNLITLSG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 DLINMPRLSG 70
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A; Cross-references: EMBL:D90908; GB:AB001339; NID:g1652725; PIDN:BAA17670.1; PID:d101840
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                  A, Cross-references: GB: AE001014; GB: AE000782; NID: 92689337; PID: 92649282; TIGR: AF1296
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T.; Zalewski,
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C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: D75617
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A;Reference number: A75250; MUID:20036896
A;Accession: D75617
A;Accession: D75617
A;Accession: D75617
A;Molecule type: DNA
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preliminary; nucleic acid sequence not shown; translation not shown
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N:Alternate names: protein s111772
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S77112
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                                                                                                                                                                                                                                                                                                                                     82 EERRPLVDVIETDNEIQVIAEMPGVNKDDI------ELNATETTLEIRAEGENR 129
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                                                                                                                                                                                                                              19;
                                                                                                                                                                          Length 174;
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A;Accession: S77112
A;Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                           27; Indels
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                                                                                                                                                                          DB 2;
                                                                                                                                                                    Score 70.5; D
Pred. No. 3;
8; Mismatches
                                                                                                                                                                    ch 15.6%;
il Similarity 28.0%;
21; Conservative
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Best Local Similarity
Matches 26; Conserv
                          A; Molecule type: DNA
A; Residues: 1-174 <KLE>
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C;Keywords: DNA repair
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Best Local S
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Ay 046 perions: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: O'Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Jul-1999
C; Accession: A47648
R; Rogalski, T.M.; Williams, B.D.; Mullen, G.P.; Moerman, D.G.
Genes Dev. 7, 141-1464, 1993
Genes Dev. 7, 141-1464, 1993
A; Title: Products of the unc-52 gene in Caenorhabditis elegans are homologous to the A; Reference number: A47648; MUID: 9339574
A; Reference number: A47648; MUID: 9339574
A; Accession: A47648
A; Accession: A47648
A; Residues: 1-2482 <ROG>
A; Corss-references: GB:L13458
A; Residues: 1-2482 <ROG>
A; Cross-references: GB:L13458
C; Superfamily: LDL receptor ligand-binding repeat homology; LDL1>
F; 190-224 / Domain: LDL receptor ligand-binding repeat homology <LDL2>
F; 233-268 / Domain: LDL receptor ligand-binding repeat homology <LDL2>
F; 231-268 / Domain: LDL receptor ligand-binding repeat homology <LEG1>
F; 1011-1058 / Domain: Laminin-type EGF-like homology <LEG2>
F; 1011-1058 / Domain: laminin-type EGF-like homology <LEG2>
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A;Introns: 32/1: 134/1; 225/1; 335/2; 450/3; 739/3; 830/3; 860/2; 1064/2; 1129/1; 115
                                     R; Baynes, C.
submitted to the EMBL Data Library, March 1997
A; Accession: 11919
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1.2482 <WIL>
A; Cross-references: EMBL: 293375; PIDN: CAB07567.1; GSPDB: GN00020; CESP: ZC101.2a
A; Experimental source: clone C38C6
A; Experimental source: clone C38C6
A; Reference number: 220375
A; Reference number: 220375
A; Residues: 1.2482 <WIL>
A; Molecule type: DNA
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llarity 28.4%; Pred. No. 1.6e+02;
Conservative 14; Mismatches 24;
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1630 FRRVSGQLNEDADE 1643
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1630 FRRVSGQLNEDADE 1643
        Accession: T19819; T27488
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A;Molecule type: DNA
A;Residues: 1-2777 <RGG>
A;Cross-retences: GB:Ll13458
C;Superfamily: LDL receptor ligand-binding repeat homology; laminin-type EGF-like homolc
C;Keywords: extracellular matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Introns: 32/1; 134/1; 225/1; 335/2; 450/3; 739/3; 830/3; 860/2; 1064/2; 1129/1; 1158/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
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A;MoLecule type: DNA
A;Residues: 1.2295 <WIZ>
A;Cross-references: EMBL:293395; PIDN:CAB07707.1; GSPDB:GN00020; CESP:ZC101.2c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein ZC101.2c - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T19820; T27489
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 PIVDAIVADNPRAVVVESPGMVKIDAPDRLTIRRETIEELTGTRFDLQ------QLQVN 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Gaps
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                                                                                                                                                                                              F;149-183/Domain: LDL receptor ligand-binding repeat homology <LDL1>F;190-224/Domain: LDL receptor ligand-binding repeat homology <LDL2>F;130-224/Domain: LDL receptor ligand-binding repeat homology <LDL2>F;233-268/Domain: LDL receptor ligand-binding repeat homology <LDL3>F;955-1002/Domain: laminin-type EGF-like homology <LEG1>F;1011-1058/Domain: laminin-type EGF-like homology <LEG2>
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Submitted to the EMBL Data Library, March 1997
A; Reference number: 219182
A; Accession: T19820
A; Status: preliminary: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Rolecule type: DNA
A; Rolecule type: DNA
A; Rolecule type: DNA
A; References: EMBL: 293375; PIDN: CAB07568.1; GSPDI
A; Experimental source: clone C38C6
R; Percy, C.
Submitted to the EMBL Data Library, March 1997
A; Reference number: 220375
A; Reference number: 220375
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Pred. No. 1.5e+02;
; Mismatches 24
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Best Local Similarity 28.4%;
Matches 21; Conservative 14
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1630 FRRVSGQLNEDADE 1643
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A; Residues: 1-138 <CAR>
A; Residues: 1-138 <CAR>
A; Cross-references: EMBL:X55394; NID:g44613; PIDN:CAA39070.1; PID:g44616
A; Cross-references: EMBL:X55394; NID:g44613; PIDN:CAA39070.1; PID:g44616
B; Fox, B.G.; Liu, Y.; Dege, J.E.; Lipscomb, J.D.
J. Biol. Chem. 266, 540-550, 1991
A; Biol. Chem. 266, 540-550, 1991
A; Title: Complex formation between the protein components of methane monooxygenase from A; Reference number: A39049; MUID:91093180
A; Accession: D39049
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A;Introns: 32/1; 134/1; 225/1; 335/2; 450/3; 739/3; 830/3; 860/2; 1064/2; 1129/1; 1158/3
2; 2613/1; 2684/1; 2757/1; 2813/3; 2863/1; 2900/3; 3084/1; 3176/1; 3250/2
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-3375 <WI2>
A; Coss.references: EMBL:293395; PIDN:CAB07708.1; GSPDB:GN00020; CESP:ZC101.2e
A; Experimental source: clone ZC101
                                                                                                                                                                                                                                                                                                                                                                                   A:Cross-references: EMBL:293375; PIDN:CAB07569.1; GSPDB:GN00020; CESP:ZC101.2e
A:Experimental source: clone C38C6
hypothetical protein 2C101.2e - Caenorhabditis elegans Cispecies: Caenorhabditis elegans Cispecies: Caenorhabditis elegans Cispecies: Caenorhabditis elegans Cispecies: To-Ct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999 Ciscossion: T19821; T27490 Ribaynes, C. Submitted to the EMBL Data Library, March 1997 A; Reference number: Z19182 A; Reference number: Z19182 A; Reference number: Z19182 A; Accession: T19821 A; Accession: T19821 A; Accession: T19821 A; Accession: T19821 A; Accession: T19821 A; Accession: T19821 A; Residues; I-3375 <WILL>
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14.7%; Score 66.5; DB 2;
Best Local Similarity 28.4%; Pred. No. 2.3e+02;
Matches 21; Conservative 14; Mismatches 24;
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submitted to the EMBL Data Library, March 1997
A; Reference number: 220375
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A; Residues: 2-32 <FOX>
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A;Gene: CESP:ZC101.2e
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Gaps
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                                                                                 Indels 12;
    Length 138;
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      DB 2;
   14.6%; Score 66; DB 2
25.5%; Pred. No. 6.6;
Live 12; Mismatches
                                                                                                                                         53 EELTGTRFDLQQLQVNLITLSGHIDEDDDEFTLS 86
                                 24; Conservative
Query Match
Best Local Similarity
Matches 24; Conserv
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us-09-430-029-6.rai

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RESULT
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Sequence 156,
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1 MAVIALKPYDFPVKDAVEKF......HKDLISFRTPGLDGLGGASF
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/pcyrUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/pcyrUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-288-988-2
US-08-288-976-2
US-08-21-756A-9
US-08-272-255-18
PCT-US95-0855-18
US-08-997-362-156
US-08-9132-619-2
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US-09-132-619-6
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US-07-928-611-22
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US-08-459-499-13
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US-09-132-619-8
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US-08-272-255-9
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Listing first 45 summaries

    protein search, using sw model

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Appl	9	Sequence	US-08-396-479B-6	٦	905	8.6	57.5	45	
Appl	ģ	Sequence	US-08-290-731C-6	7	1336	8.7	58	44	
Appl	7	Sequence	US-08-290-731C-2	7	1319	8.7	58	43	
Appl	5,	Sequence	US-08-690-473-2	7	1298	8.7	28	42	
Appl	8	Sequence	US-08-494-168-8	Н	549	8.7	28	41	
App1	, ,	Sequence	US-08-869-477-7	~	482	8.7	58	40	
Appli	′,	Sequence	US-08-142-439A-7	Н	482	8.7	. 58	39	
Appli	'n	Sequence	US-07-792-885A-1	-	482	8.7	28	38	
Appli	2	Sequence	PCT-US94-02389-2	4	360	8.8	Э	37	
Appli	2,	Sequence	US-08-205-506A-2	-	360	8.8	58.5	36	
Appli	2,	Sequence	PCT-US93-03027-2	4	558	6.8	59	35	
App	13,	Sequence	PCT-US92-11107-13	4	542	8.9	29	34	
Appli	ω,	Sequence	US-08-328-809-8	П	542	8.9	59	33	
App.	13,	Sequence	US-08-258-442-13	Н	542	8.9	59	32	
App	13,	Sequence	US-07-814-964-13	-	542	8.9	59	31	
App	22,	Sequence	PCT-US93-07370-22	7	467	8.9	29	30	
App.	22,	Sequence	US-08-487-811A-22	ď	467	8.9	59	29	

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Sequence 5, Application US/08319387
Patent No. 5543317
GENERAL INFORMATION:
APPLICANT: Shields, Malcolm S.
APPLICANT: Francesconi, Stephen C.
TITLE OF INVENTION: Microbial Degradation of Trichloroethylene, TITLE OF INVENTION: Dichloroethylenes and Aromatic Pollutants NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,387
                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/167,457
FILING DATE: 15-DEC-1993
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/694,718
FILING DATE: 02-MAY-1991
TACSTFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: UW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 93 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide US-08-319-387-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                      US-08-319-387-5
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APPLICANT:
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                                                             US-08-290-301-2
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                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                    A method to increase the trehalose content of organisms by transforming them with the structural genes for the short and long chains yeast trehalose synthase.
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     55.6%; Score 370; DB 1; Length 93; 67.7%; Pred. No. 8e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                         18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS
SOFTWARE: WP5.1 file exported as DOS text file
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/841,997A
FILING DATE: 19920228
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/836,021
FILING DATE: February 14, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 78.5; DB 1;
Pred. No. 0.34;
19; Mismatches 28;
                                         12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: Finland
ZIE: SF-00101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb
COMPUTER: IBM PC/XT/AT_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 RVEWF -- - RSGEPWAPDPAK SLAGNGLGHKDLI 103
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                                                                                                                                                           61 YGYHPDFAKIDWDRVEWFRSGEPWAPDPAKSLA 93
                                                                                                                                                                               20085A
                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Londesborough, John
APPLICANT: Vuorio, Outi
TITLE OF INVENTION: A method to |
TITLE OF INVENTION: Structural ge |
TITLE OF INVENTION: Structural ge |
TITLE OF INVENTION: yeast trehalc |
WINMER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                            Sequence 2, Application US/07841997A
Patent No. 5422254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Mary E. Gormley
REGISTRATION NUMBER: 34409
REFERENCE/DOCKET NUMBER: $200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)659-2930
TELEFAX: (202)887-0357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 440142
INFORMATION FOR SEQ ID NO: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 11.8% Best Local Similarity 24.7%; Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acids
TYPE: AMINO ACID
                                         63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 KDLLEKFNAVPIFLSDE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Alko Ltd
STREET: PO BOX 350
Query Match
Best Local Similarity
Matches 63; Conserva
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HYPOTHETICAL:
                                                                                                                                                                                                                                                        RESULT 2
US-07-841-997A-2
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APPLICANT: Welln, Bjorn
APPLICANT: Wandel, Abul
TITLE OF INVENTION: Increasing the trehalose content
TITLE OF INVENTION: of organisms by transforming them with combinations of
TITLE OF INVENTION: the structural genes for trehalose synthase.
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS
SOFTWARE: WP5.1 file exported as DOS text file
CURRENT APPLICATION DATA:
AUGUSTALOATION NUMBER: US/08/290,301
FILING DATE: 15 August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.8%; Score 78.5; DB 1; 24.7%; Pred. No. 0.34;
                                                                                                                                                                                                                                                                                                                                                                                                STATE:
COUNTRY: Finland
ZIP: SF-00101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb
COMPUTER: IBM PC/XT/AT
COMPUTER: WP5.1 file exported as DOS text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 RVEWF---RSGEPWAPDPAKSLAGNGLGHKDLI 103
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APPLICATION NUMBER: PCT/F193/00049
FILING DATE: 15 February 1993
APPLICATION NUMBER: 07/841,997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/841,997
FILING DATE: 28 February 1992
APPLICATION NUMBER: 07/836,021
FILING DATE: 14 February 1992
ATTORNEY/AGENT INFORMATION:
NAME: Kubovcik, Ronald J.
NAME: Lydon, James C.
REGISTRATION NUMBER: 25,401
REGISTRATION NUMBER: 30,082
REGISTRATION NUMBER: 1400-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 467-6300
                                                                                             APPLICANT: Tunnela, Outi
APPLICANT: Palva, Tupio
APPLICANT: Holmstrom, Kjell-Ove
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FI 943133
Sequence 2, Application US/08290301
Patent No. 5792921
                                                                         Londesborough, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202) 467-6300
TELEFAX: (202) 466-2006
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: Polypeptide HYPOTHETICAL: Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 KDLLEKFNAVPIFLSDE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 495 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23; Conservative
                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Alko Ltd.
STREET: PO BOX 350
CITY: Helsinki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                   GENERAL INFORMATION:
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14 KDAVEKFPAPLLYVCWENHLMFPAPFCLPLPPDMPFGALAGDVLPPVYGYHPDFAKIDWD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 495;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/08221750A
Patent No. 5643747
GENERAL INFORMATION:
APPLICANT: Baker, Steven M.
APPLICANT: Deich, Robert A.
TITLE OF INVENTION: Genes for the Export of Pertussis TITLE OF INVENTION: Holotoxin NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: LIUPPY UISK
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,750A
FILING DATE: 31-MAR.1994
CLASSIFICATION 1435
PRIOR APPLICATION 1435
PRIOR APPLICATION NUMBER: US/08/031,619
FILING DATE: 15-MAR-1993
ATTONEY/AGERT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington COUNTY: MA COUNTY: MA
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,976
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; DB 2;
0.34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 ENAWFGYNEANOTFTNEIAKT-----MNHNDLI 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 78.5;
Pred. No. 0.
                                                                                                                                                                                          NAME: Fussey, Shelley P.M.
REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: UTSD:481/FUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: ACC93-01A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.8%;
24.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 KDLLEKFNAVPIFLSDE----
                                                                                                                                                                                                                                                                                                                                                                                      495 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 24.74
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                       TELEX: n/a INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
US-08-588-976-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 02173
                                                                                                                                                                                                                                                                                                   TELEFAX:
TELEX: n/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
US-08-221-750A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28; Indels
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: DEAD PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION WIMBER: US/08/588,983
FILING DATE: CONCURTENTLY herewith
THENCE DATE: CONCURTENTLY HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Christopher B. Newgard, et al.
TITLE OF INVENTION: Methods and Compositions for
TITLE OF INVENTION: Inhibiting Hexokinase
                                                        Sequence 2, Application US/08588983;
Patent No. 5854067;
GENERAL INFORMATION:
TITLE OF INVENTION: Methods and Compositions;
TITLE OF INVENTION: for Inhibiting Hexokinase;
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALROId, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.8%; Score 78.5; DB 2; 24.7%; Pred. No. 0.34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 RVEWF---RSGEPWAPDPAKSLAGNGLGHKDLI 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Fussey, Shelley P.M.
REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: UTSD:424/FUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFRAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. BOX 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08588976
Patent No. 5891717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: n/a
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 77210
COMPUTER READABLE FORM:
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Best Local Similarity
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                                                                                                                                                                                                                                                                               Houston
                                                                                                                                                                                                                                                                                                                       nS
                                                                                                                                                                                                                                                                                               STATE: TX
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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US-08-588-976-2
                            RESULT 4
US-08-588-983-2
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APPLICANT: WATSON, JAMES D.
APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                            APPLICANT: Cashmore, Anthony R.
APPLICANT: Ahmad, Margaret
APPLICANT: Lin, Chentae
APPLICANT: Lin, Chentae
TITLE OF INVENTION: Blue Light Photoreceptors and Methods of
TITLE OF INVENTION: Using the Same
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & Norris
STREET: One Liberty Place, 46th floor
                                                            20 VQSFNADLLYEPWEVVDDEGQSFTWF-APFWNRCLSMPYDP----AAPLLPP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
                                 17 VEKFPAPLLYVCWE-----NHLMFPAPF---CLPLPPDMPFGALAGDVLPP
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 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08565
12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Law Offices of Ann W. Speckman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 62; DB 4; Pred, No. 39; 4; Mismatches
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,255
FILING DATE: 08-UUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn
REGISTRATION NUMBER: 36,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UPN-1795
                                                                                                                          RESULT 8
FOT-10595-08565-18
Sequence 18, Application PC/TUS9508565
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-997-080-156; Sequence 156, Application US/08997080; Patent No. 5968524; CENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: UI
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPAN: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
LENGTH: 655 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.3%;
Best Local Similarity 39.6%;
Matches 21; Conservative
21; Conservative
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STATE:
Matches
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                                                                                                                                                                                                                                                                                                                        35 -----AGDVLPPVYGYHPDFAKI 70
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STREET: One Liberty Place, / 46th floor
                                                                                                                                                                                                                                                                                                                                                                                                                   71 DWDRVEW--FRSGEPW-----APDPAKSLAGNGLGHKDLISFR-TPGLDGLGGAS 117
                                                                                                                                                                                                               71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Photoreceptors and Methods of
                                                                                                                                                                             Length 273;
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                                                                                                                                                                                                                 Indels
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Pred. No. 39;
                                                                                                                                                                           Score 71.5; D
Pred. No. 1;
20; Mismatches
                                                                                                                                                                                                                                                   3 VIALKPYDFPVKDAVEKFPAPLLYVCWENHLM----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18, Application US/08272255
Patent No. 5824859
GENERAL INFORMATION:
APPLICANT: Cashmore, Anthony R. APPLICANT: Ahmad, Margaret
APPLICANT: Lin, Chentao
TITLE OF INVENTION: Blue Light Phot
TITLE OF INVENTION: Using the Same
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA: | APPLICATION DATA: | APPLICATION NUMBER: US/08/272,255 FILING DATE: 08-JUL-1994 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn
REGISTRATION NUMBER: 36/317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION
                                                                                                                                                                           Query Match 10.7%;
Best Local Similarity 21.6%;
Matches 38; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: (18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.68;
                                               : 273 amino acids
amino acid
           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 655 amino acida
amino acid
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                                                                                                 ; MOLECULE TYPE: protein US-08-221-750A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-272-255-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Philadelphia
                                                                                    linear
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Best Local Similarity
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                                                                                  TOPOLOGY:
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                                             LENGTH:
                                                                 TYPE:
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATE:
PRIOR APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
APPLICATION NUMBER: 10.5. Patent Application No. 5985287 08/705,347
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 17,007
REFERENCE/DOCKET NUMBER: 11000.1002c2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----PWAPDPAKSLAGNGLGHKDLISFRTPGL--DG 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 495;
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Patent No. 5958697
GENERAL INFORMATION:
APPLICANT: Shan, Bei
APPLICANT: Nitta, Masahiro
FITLE OF INVENTION: CYP7 Promoter-Binding Factors
FITLE REFERENCE: 197-013
CURRENT APPLICATION NUMBER: US/09/132,619B
CURRENT FILING DATE: 1998-08-11
FEALLER PELICATION NUMBER: 60/067,708
FARLIER FILING DATE: 1997-12-08
NUMBER OF SEQ ID NOS: 30
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                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CUSTURARE: FastSED for Windows Version 2.0
CUSTENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHRRACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.2%
Best Local Similarity 22.3%
Matches 27; Conservative
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Matches 28; Conservative
           Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
US-08-997-362-156
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US-09-132-619-2
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US-09-132-619-2
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LENGTH: 495
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Patent No. 5985287
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Hyama, Jun
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Scott, Linda
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | : | : | : | : | 37 SGRATYVVAGEGADEFEGTLELGYHVGFPWS-----LGVGIN----FSYTTPNITYDG 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 9.2%; Score 61; DB 2; Length 336; Best Local Similarity 23.0%; Pred. No. 22; Matches 28; Conservative 10; Mismatches 28; Indels
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                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
OFRATING SYSTEM: DOS
SOFTWARE: FASTSEC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                           11000.1007
                                                                                                                                                                                                                                                                                                                                                                   ATTORIEN DAIL:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/POCKET NUMBER: 1100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX:
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
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                           Seattle
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                                                                   USA
                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                 FILING DATE
                                                                                     98121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY:
US-08-997-080-156
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                                                                   COUNTRY:
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STATE:
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Sequence 6, Application US/09132619B Patent No. 5958697
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94010
                                                                                                                                                                                                                                                         LENGTH: 541
                                                                                                                                                                                                                                                                                                                  US-09-132-619-6
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                                                                     47 MPFGALAGDVLPPVYGYHPDFAKIDWDRVEWFRSGEPWAPDPAKSLAGNGLGHKDLISFR 106
                                                                                              --RAIKSEYPDPYTSSPESIMGYSYMDSYQ 248
                                   --NHAALPPTDYDRSPFVTSPISMTMP-- 204
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Pred. No. 36;
17; Mismatches 37; Indels
                                                                                                                                                                                                                                                                 Sequence 2, Application US/09282803B
Patent No. 6027901
GENERAL INFORMATION:
APPLICANT: Shan, Bei
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBORDUGH
STATE: CALLFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-50S/MS;DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/282,803B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---PLLYVCWENHLMFP---
                            153 VIQAMPSDLTISSAIQNIHSASKGLPL---
                                                                                                205 -PHGSLQG---YQTYGHFPS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 797
REFERENCE/DOCKET NUMBER: 797
TELECOMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEPHONE: (650) 343-4341
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 495 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 22.3%
Matches 27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94010
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                         US-09-282-803B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-282-803B-2
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                                                                                                                                                                                 249 T 249
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US-09-132-619-6
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47 MPFGALAGDVLPPVYGYHPDFAKIDWDRVEWFRSGEPWAPDPAKSLAGNGLGHKDLISFR 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Shan, Bei
APPLICANT: Nitta, Masahiro
APPLICANT: Nitta, Masahiro
APPLICANT: Nitta, Masahiro
APPLICANT: Nitta, Masahiro
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
GENERAL INFORMATION:
APPLICANT: Shan, Bei
APPLICANT: Nitta, masahiro
TITLE OF INVENTION: CYPP Promoter-Binding Factors
FILE REFERENCE: T97-013
                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.2%; Score 61; DB 2, 22.3%; Pred. No. 40; ive 17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE CITY: HILLEBOROUGH STATE: CALLFORNIA COUNTRY: USA
                                                                                                                     CURRENT APPLICATION NUMBER: US/09/132,619B CURRENT FILING DATE: 1998-08-11 EARLIER APPLICATION NUMBER: 60/067,708 EARLIER FILING DATE: 1997-12-08 NUMBER OF SEQ ID NOS: 30 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/282,803B
FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION UNDHER: 36,627
REFERENCE/DOCKET NUMBER: 197-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEPAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Floppy disk
IBM PC compatible
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Best Local Similarity 22.38
Matches 27; Conservative
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                                                                                                                                                                                                                                                                                                  251 -PHGSLQG---YQTYGHFPS------RAIKSEYPDPYTSSPESIMGYSYMDSYQ 294
                                                                                                                                                    Gaps
                                                                                                                                                                                    3 VIALKPYDFPVKDAVEKFPA----PLLYVCWENHLMFP------APFCLPLPPD 46
                                                                                                                                                  40;
                                                                                                       Query Match 9.2%; Score 61; DB 3; Length 541; Best Local Similarity 22.3%; Pred. No. 40; Matches 27; Conservative 17; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08749902
Fatent No. 5985635
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
TITLE OF INVENTION: PROTEIN KINASES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0150 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-885-0555
TELERAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US

ZIP: 94304
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,902
FILING BATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acids
TYPE: amino acid
STRAMDENNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-282-803B-6
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Gaps

23;

31; Indels

Query Match
8.9%; Score 59.5; DB 2;
Best Local Similarity 26.2%; Pred. No. 53;
Matches 22; Conservative 8; Mismatches 31;

Length 495;

Search completed: September 26, 2000, 20:22:46 Job time: 3820 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

September 26, 2000, 20:24:21 Run on:

; Search time 82.1 Seconds (without alignments) 88.945 Million cell updates/sec

666
1 MAVIALKPYDFPVKDAVEKF......HKDLISFRTPGLDGLGGASF 118 US-09-430-029-6 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

178050 seqs, 61884766 residues Searched:

178050 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

pir1:* pir2:* pir3:* PIR_64:* % w ₹ Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	apyconom-c lonedu				chlorophyll a/b-bi	NADH dehydrogenase	alpha,alpha-trehal	VirB9 homolog - Bo	phosphoenolpyruvat	viral proteinase -	sex-determining pr	conserved hypothet	fomF protein - Str	heat shock transcr	hypothetical prote	transcription fact	hypothetical prote		hypothetical prote	proline-rich prote	probable cell divi	diaphanous-related	glyceraldehyde-3-p	beta-fructofuranos	ropy-2 protein [im	interleukin-11 rec	paired box transcr	NADH dehydrogenase	isobutyryl-CoA mut
SUMMARIES	a l	E37831	544307	S47291	A45730	S46295	S52261	S34979	D47301	S69546	S52216	S26045	T40809	S60207	S61459	G25035	S12788	T43464	T46476	T16836	T06076	G75523	T17454	T44939	S57951	T46589	137891	A57374	JE0092	T43706
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,	% Query Match	32.4	31.9	21.5	19.1	12.7	11.8	10.9	10.7	10.7	10.7	10.2	10.2	10.1	10.0	10.0	10.0	10.0	10.0	6.6	6.6	6.6	6.6	9.8	9.8	8.6	9.8	9.8	9.8	9.8
	Score	215.5	212.5	143	127	84.5	78.5	72.5	71.5	71.5	7.1	89	99	67.5	66.5	66.5	66.5	66.5	66.5	99	99	99	99	65.5	65.5	65.5	65	65	65	65
	Result No.		7	т	4	S	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote	chitinase (EC 3.2.	chitinase (EC 3.2.	stilbene synthase	stilbene synthase	transforming prote	hypothetical prote	probable quinone o	NADH dehydrogenase	hypothetical prote	isobutyryl-CoA mut	hypothetical prote	hypothetical prote	complement subcomp	hypothetical prote	hairless protein -
B75433	839979	S40414	S68772	S68773	S15704	F70799	S57612	A39362	T33800	T46549	H64447	T31487	CIHURB	T14756	148378
7	7	7	7	7	?	7	7	Н	~	7	~	~	Н	7	~
131	339	340	396	396	437	169	342	464	472	266	622	069	705	990	1182
9.7	9.7	9.7	9.7	9.7	9.7	9.6	9.6	9.6	9.6	9.6	9.6	9.6	9.6	9.6	9.6
64.5	64.5	64.5	64.5	64.5	64.5	64	64	64	64	64	64	64	64	64	64
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

DECITE 1
E37831
phenol 2-monooxygenase (EC 1.14.13.7) chain P4 - Pseudomonas sp. (strain CF600)
C;Species: Pseudomonas sp.
C;Date: 10-Sep-1999 #Sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: E37831
R; Nordlund, I.; Powlowski, J.; Shingler, V.
J. Bacteriol. 172, 6826-6833, 1990
A; Title: Complete nucleotide sequence and polypeptide analysis of multicomponent phen
A; Reference number: A37831; MUID:91072230
A; Accession: E37831
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-119 <nor></nor>
A; Cross-references: GB:M60276; GB:M37764; NID:q151449; PIDN:AAA25943.1; PID:q151454
C; Superfamily: phenol 2-monooxygenase component O
C; Keywords: oxidoreductase

ä Gaps ï Length 119; Indels Ouery Match 32.4%; Score 215.5; DB 1; Best Local Similarity 37.6%; Pred. No. 1.1e-15; Matches 44; Conservative 18; Mismatches 54;

1 MAVIALKPYDFPVKDAVEKFPA-PLLYVCWENHLMFPAPFCLPLPPDMPFGALAGDVLPP 59 ò qq

60 VYGYHPDFAKIDWDRVEWFRSGEPWAPDPAKSLAGNGLGHKDLISFRTPGLDGLGGA 116 ò g

PRESOURT 2
S44307
phenol 2-monooxygenase (EC 1.14.13.7) component O - Pseudomonas putida
NiAlternate names: phenolhydroxylase chain E
C; Species: Pseudomonas putida
C; Species: Pseudomonas putida
C; Species: Pseudomonas putida
C; Sate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: F58972: S54764; S44307; S44418
R; Ny. L.C.; Shingler, V.; Sze, C.C.; Poh, C.L.
Gene 151, 29-36, 1994
A; Title: Cloning and sequences of the first eight genes of the chromosomally encoded
A; Reference number: A58972; MUID: 95129877
A; Accession: F5897
A; Accession: F5897
A; Status: preliminary
A; Molecule type: DNA
A; Status: preliminary
A; Molecule type: DNA
A; Status: preliminary
A; Molecule type: DNA
A; Status: preliminary
A; Molecule type: DNA
A; Status: preliminary
A; Mullecule type: DNA
A; Status: preliminary
A; Cross-references: EMBL: X79063; NID: 9483477; PIDN: CAA55664.1; PID: 9483482
A; Cross-references: EMBL: X79063; NID: 9483477; PIDN: CAA55664.1; PID: 9483482
A; Rrimental source: strain P35X (NCBI 9869)
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
B; Herrmann, H.; Mueller, C.; Schmidt, I.; Mahnke, J.; Petruschka, L.; Hahnke, K.
Mol. Gen. Genet. 247, 240-246, 1995

```
A;Title: Complete nucleotide sequence of tbub, the gene encoding phenol/cresol hydrox A;Reference number: A45730; MUID:93015703
A;Reference number: A45730
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-671 <KUK>
A;Residues: 1-671 <KUK>
A;Cenetics: A;Genetics: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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27.78;
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35.1%;
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C,Superfamily: chlorophyll
C,Keywords: photosystem I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Grohmann, L.; Thieck, O. submitted to the EMBL Data A;Reference number: S52261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 -----DLGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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N.Alternate names: phenol hydroxylase
N.Alternate names: phenol hydroxylase
N.Alternate names: phenol hydroxylase
C.Species: Acinetobacter calcoaceticus
C.Species: Acinetobacter calcoaceticus
C.Accession: S70084: $47291
R.Ehrt, S.; Schirmer, F.; Hillen, W.
Mol. Microbiol. 18, 13-20, 1995
A.Title: Genetic organization, nucleotide sequence and regulation of expression of genes
A.Title: Genetic organization, nucleotide sequence and regulation of expression of genes
A.Title: Genetic organization, nucleotide sequence not shown
A.Status: nucleic acid sequence not shown; translation not shown
A.Status: nucleic acid sequence not shown; translation not shown
A.Status: nucleic acid sequence was submitted to the EMBL Data Library, September 1994
A.Steperimental source: strain NCIB#250
A.Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1994
        phenol degradation genes of Pseudomonas putida
                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-9, 'T', 11-40, 'G', 42-119 <HE2>
A; Cross-references: EMBL: X80765; NID: 9527546; PIDN: CAA56744.1; PID: 9527551
A; Experimental source: strain H
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
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                                                                                                                      Status: preliminary; nucleic acid sequence not shown; translation not shown
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C;Species: Pseudomonas pickettii
C;Species: Pseudomonas pickettii
C;Bate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999
C;Accession: A45730
R;Kukor, J.J.; Olsen, R.H.
J. Bacteriol. 174, 6518-6526, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAVIALKPYDFPVKDAVEKFPA-PLLYVCWENHLMFPAPFCLPLPPDMPFGALAGDVLPP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MTVQAIVEKYQFEPLDLQQNYGENMLLFIGWDHHTLFCSAHAFVVSPKQSLQALIDGQIQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 VYGYHPDFAKIDWDRVEWFRSGEPWAPOPAKSLAGNGLGHKDLISFRTPGLDGLGGA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 PVYGYHPDFAKIDWDRVEWFRSGEPWAPDPAKSLAGNGLGHKDLISFRTPGLDGLGG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; DB 1;
2.2e-15;
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Pred. No. 4.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: phlE; phhO
C;Superfamily: phenol 2-monooxygenase component O
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.9%; Score 212.5;
36.8%; Pred No. 2.2e
iive 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l8; Mismatches
    Title: Localization and organization of Reference number: S54761; MUID:95272534
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Local Similarity 31.6%;
les 37; Conservative 1
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Best Local Similarity
Matches 43; Conserv
Localization
                                                                             A; Accession: S54764
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NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) flavoprotein 1 precursor - potato N.Alternate names: mitochondrial complex I 51K chain; NADH dehydrogenase (ubiquinone) C;Species: Solanum tuberosum (potato) C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 11-Jun-1999 C;Accession: S52261 R;Grohmann, L.; Thieck, O.
                                                         .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chlorophyll a/b-binding protein type II - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 01-Feb-1995 #sequence_revision 19-Jan-1996 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-271 <2HA>
A; Cross-references: EMBL:U03395; NID:g541564; PIDN:AAA57542.1; PID:g541565
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A;Molecule type: mRNA
A;Residues: 1-487 <GRO>A;Residues: 1-487 <GRO>A;Cross-references: EMBL:X83999; NID:g639833; PIDN:CAA58823.1; PID:g639834
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                                                         :99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 271;
  Length 671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: S46295
C;Accession: S46295
R;Zhang, H.; Wang, J.; Goodman, H.M.
Plant Mol. Biol. 25, 551-557, 1994
A;Title: Differential expression in Arabidopsis of Lhca2, a PSI
A;Reference number: S46295; MUID:94325479
A;Accession: S46295
A;Status: nucleic acid sequence not shown
                                                      28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
Score 127; DB 2;
Pred. No. 1.5e-05;
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0.16;
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                                                      13; Mismatches
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Pred. No. 0.
  Score 127;
                                                                                                                                                                                                                                                                                                                                  92 ----LAGNGLGHKDLISFRTPGLDGLG 114
                                                                                                                                                                                                                                                                                                                                                                                   297 EGRVFLAGDA-----RHRHPPLTGIG 317
                                                                                                            1 MAVIA-LK--PYDFPVKDAVEKFPAPL----
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us-09-430-029-6.rpr

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A;Molecule type: protein
A;Residues: 63-64,'X',66-71;196-200;223-244;280-283;294-298;304,'X',306-313,'X',315-3
R;Feldmann, H.
                                                                                                                                                                                                                                                                                                                                                                                              A,Accession: S22259
A;Molecule type: DNA
A;Residues: 1-128, FG/,131-495 <GON>
A;Residues: 1-128, FG/,131-495 <GON>
A;Coss-references: EMBL:X61275; NID:g3539; PIDN:CAA43580.1; PID:g3540
B;Bell, W.; Klaassen, P.; Ohnacker, M.; Boller, T.; Herweijer, M.; Schoppink, P.; van Eur. J. Blochem. 209, 951-959, 1992
A;Title: Characterization of the 56-KDa subunit of yeast trehalose-6-phosphate syntha
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C;Keywords: glycosyltransferase; hexosyltransferase; trehalose biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Accession: $27249
A, Molecule type: mRNA
A, Residues: 1-74, "w',76-100,"L',102-103,"W',105-216,'S',218-287,'L',289-495 <BEL>
A, Residues: 1-74, "w',76-100,"L',102-103,"W',105-216,'S',218-287,'L',289-495 <BEL>
A, Cross-references: EMBL:X68314; NID:g4626; PIDN:CAA48296.1; PID:g4627
R; Vuorio, O.E.; Kalkkinen, N.; Londesborough, J.
Eur. J. Blochem. 216, 849-861, 1993
A; Title: Cloning of two related genes encoding the 56-kDa and 123-kDa subunits of A; Reference number: $38868; MUID:94009048
A; Accession: S45994
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 291-495 cFEL>
A; Cross-references: EMBL: 235995; MIPS:YBR126c
R; Gonzalez, M.I.; Stucka, R.; Blazquez, M.A.; Feldmann, H.; Gancedo, C.
R; Sast B, 183-192, 1992
A; Title: Molecular cloning of CIFI, a yeast gene necessary for growth on glucose.
A; Reference number: S22259; MUID: 92245756
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J. Biol. Chem. 264, 1775-1778, 1989
A;Title: A conserved gene encoding the 57-kDa subunit of the yeast vacuolar lak;Reference number: A31487; MUID:89109197
A;Reference number: A31487
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A;Residues: 366-495 <NEL>
A;Cross-references: EMBL:J04450; NID:g171121; PIDN:AAA66892.1; PID:g808825
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A;Cross-references: SGD:S0000330; MIPS:YBR126c
A;Map position: 2R
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A,Residues: 291-495 <FE2>
A,Cross-references: EMBL:X78993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Molecule type: DNA
A; Residues: 1-495 < MOD:
A; Residues: 1-495 < MOD:
A; Residues: 1-495 < MOD:
A; Cross-references: EmBL:X68496; NID:94628; PIDN:CAA48510.1; PID:94629
B; Becam, A.M.; Cullin, C.; Grzybowska, E.; Lacroute, F.; Nasr, F.; Ozier-Kalogeropoulos, Yeast 10(Suppl.A). S1-S11, 1994
A; Title: The Sequence of 29.7kb from the right arm of chromosome II reveals 13 complete A; Reference number: S46569; MUID:94378717
A; Reference number: S46569; MUID:94378717
A; Accession: S46569
A; Molecule type: DNA
A; Residues: 1-495 < MEZ>
A; Cross-references: EMBL:X75891; NID:9496856; PIDN:CAA53485.1; PID:9496857
B; Becam, A.M.; Herbert, C.J.; Nasr, F.; Slonimski, P.P.; Zagulski, M.
A; Reference number: S45995
A; A; Accession: S45995
                                                                                              A:Pathway: oxidative phosphorylation
C:Superfamily: NADH dehydrogenase (ubiquinone) chain F; NADH dehydrogenase (ubiquinone)
C:Superfamily: NADH dehydrogenase (ubiquinone) chain; membrane-associated complex;
E:92-470/Domain: NADH dehydrogenase (ubiquinone) I chain F homology <NUOF>
F:110-119/Region: NADH binding motif
F:223-238/Region: FMN binding motif
F:402,405,408,448/Binding site: 4Fe-4S cluster (Cys) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-495 <BEC.
A;Cross-references: EMBL:235995; NID:9536410; PIDN:CAA85083.1; PID:9536411; MIPS:YBR1260
R;Cannon, J.F.; Pringle, J.R.; Fiechter, A.; Khalil, M.
Genetics 136, 485-503, 1994
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A; Accession: $47858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 PQPTPPPPPPERTHEGGLKDEDRIFTNLYGLHDPYLKGAMKRGDWYRTKDLVIKGSDWIV 100
                                                      catalyzes the reduction of ubiquinone to ubiquinol by NADH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 PAPFCLPLPPDMP-FGALAGD--VLPPVYGYHPDFAKIDWDRVEWFRS-----GEPWAP 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-495 <VAN>
A; Residues: 1-495 <VAN>
A; Residues: EMBL:X67499; NID:g3741; PIDN:CAA47834.1; PID:g3742
B; McDougall, J.; Kaasen, I.; Strom, A.R.
submitted to the EMBL Data Library, September 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 78.5; Di
Pred. No. 1.3;
9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.8%;
27.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 11.8
Best Local Similarity 27.2
Matches 25; Conservative
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A; Accession: S31310
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101 NEMKK-----
                                                           A; Description:
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H+-ATPase

4

23; Gaps

Length 495; Indels

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A;Cross-references: FlyBase:FBgn0012404
A;Introns: 11/3; 134/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.7%;
23.4%;
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ilarity 33.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL: X79983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 10.77
Best Local Similarity 23.43
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: genomic RNA
A;Residues: 1-522 <CAM>
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hes 20; Conserv
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Best Local S
Matches 20
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C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 22-Jun-1999
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 22-Jun-1999
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 22-Jun-1999
C;Accession: S69546
Biochem. J. 315, 807-814, 1996
Biochem. J. 315, 807-814, 1996
A;Title: Molecular cloning, sequencing and expression of the cDNA of the mitochondrial A;Reference number: S69546; MUID: 96220691
A;Reference number: S69546
A;Residues: preliminary
A;Residues: 1-640 <MOD>
A;Residues: 1-640 <MOD>
A;Residues: 1-640 <MOD>
A;Residues: 1-640 <MOD>
A;Residues: 1-640 <MOD>
A;Residues: 1-640 <MOD>
A;Residues: 1-640 <MOD>
C;Genetics:
C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Cenetics: C;Genetics: C;Cenetics: C
                                                                                                                         R;Weiss, A.A.; Johnson, F.D.; Burns, D.L!
Proc. Natl. Acad. Sci. U.S.A. 90, 2970-2974, 1993
A;Title: Molecular characterization of an operon required for pertussis toxin secretion.
A;Reference number: A47301; MUID:93219406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphoenolpyruvate carboxykinase (5TP) (EC 4.1.1.32) precursor, mitochondrial - human
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8
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                               C;Species: Bordetella pertussis
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |: :| || : : | | | | | || || 83 VLYIKAKSFPAQGSPAQAPEPGL---WNTULLVKTDRRLYDFDLVLASADAATPQALQRS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Note: sequence extracted from NCBI backbone (NCBIN:128775, NCBIP:128780)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 RMAYRLOFRYPAAPQAASRASPVGPAVPAGALNRRYAMOVGNGSDGIAPIAAY----- 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 -----GYHPDFAKIDWDRVEWFRS-----GEP---WAPDPAKSLAGNGLGHKDLI 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -AGDVLPPVYGYHPDFAKI 70
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Pred. No. 9.7;
16; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 10.7%; Score 71.5; DE Best Local Similarity 21.6%; Pred No. 3.6; Matches 38; Conservative 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 VIALKPYDFPVKDAVEKFPAPLLYVCWENHLM-----
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   pertussis
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Best Local Similarity 25.4%;
Matches 34; Conservative |
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135 MSPADFQ-RAVDERFPG---
                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: nucleic acid
A; Residues: 1-273 <WEI>
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SFGS----GYGGNS 257
- Bordetella
                                                                                                                                                                                                                                                                                               A; Accession: D47301
A; Status: preliminary
                                                                                          C; Accession: D47301
                                                                                                                                                                                                                                                                    A; Contents: BP338
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RESULT 10

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conserved hypothetical zinc-finger protein - fission yeast (Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe C; Species: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change O3-Dec-1999 C; Accession: T40809 R; Beck, A.; Reinhardt, R.; Lyne, M.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, October 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Drosophila hydel
C; Date: 19-Jul-1996 #text_change 17-Mar-1999
C; Date: 19-Jul-1996 #text_change 17-Mar-1999
C; Accession: S26045
R; O'Neil, M.T.; Belote, J.M.
Genetics 131, 113-128, 1992
A; Title: Interspecific comparison of the transformer gene of drosophila reveals an un A; Reference number: S26044; MUID: 92275311
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viral proteinase - rabies virus
C;Species: rabies virus
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Aug-1998
C;Accession: S52216
R;Camacho, A: Tabaro, E
submitted to the EMBL Data Library, June 1994
A;Reference number: S52215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 HLMFPAPFCLPLPPD-MPFGAL------AGDVLPPVYGYHPDFAKIDWDRVEWFR 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sex-determining protein transformer - fruit fly (Drosophila hydei)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type:.DNA
A;Residues: 1-201 <OND
A;Cross-references: EMBL:X66931; NID:97457; PID:97458
A;Note: the authors did not translate the codon for residue 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |: :| |: | || :| || 349 HVRYPTPYYAPAPPQLLPPGAVVGHPHPHPHPAGALYPPMYAPQPGL---
                                                                                                                                                                                                                                                                                                                                                        A;Note: the source is designated as pseudorables virus C;Superfamily: varicella-zoster virus gene 33 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
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Pred. No. 5.9;
7; Mismatches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: 221949
A;Accession: T40809
A;Status: prellminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-482 <BEC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Score 71; DB 3; Pred. No. 8.7; 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 SGEPWAPDPAKSLAGNGLGHKDLISFRTPGLDGL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               397 ----HAPPPSP------VAHAVPALPGL 414
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S

transcription factor; t

5,

Gaps

39;

Length 94; Indels

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"hypothetical protein 2 - Escherichia coli plasmid Colla Cispecies: Escherichia coli Cispecies: Escherichia coli Cispecies: Escherichia coli Cispecies: 24-Jan-1988 #sequence_revision 24-Jan-1988 #text_change 18-Jun-1993 C;Accession: G25035
Bacteriol. 168, 228-236, 1986
A;Title: DNA and amino acid sequence analysis of structural and immunity genes of characterice number: A91822; MUID:87008385
A;Reference number: A91822; MUID:87008385
                                                                                                                                                                                                                                                                                                    1 MAVIALKPYDF---PVKDAVEKFPA-PLLYVCWENHIMFPAPFCLPLPPDMPFGALAGDV 56
                                                                                                                                                                                                                                                                                                                                  20 FPAPLLYVCWENHLMFPAPFCLPLPPDMPF-----GALAGDVLPPVYGYHPDFAKIDW, 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 YAPPLIRILWRIGIRLP-----PEMPFWQVTVLTGGLWG------ISW 49
       A;Gene: hsfc
C;Function:
A;Description: transcriptional activator of hsp genes
C;Superfamily: HSF DRA-binding domain homology
C;Reywords: DNA binding; heat shock; leucine zipper; nucleus; tr
F;4-94/Domain: HSF DNA-binding domain homology (fragment) <HSF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 DRVEWFRSGEPWAPDPAKSLAGNGLGHKDLISFRTPGLDGLGGASF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCVMWFTY---WGP-----SGMVAGEAIISITGGFLFGLCMASF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches 33;
                                                                                                                                                                                                       Score 66.5; DB
Pred. No. 3.5;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.0%; Score 66.5; 29.2%; Pred. No. 3.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: September 26, 2000, 20:24:24
Job time: 3648 sec
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                                                                                                                                                                                                                                                                                                                                                                                                 57 LP-PVYGYHPDFAKIDWDRVEWFRSG 81
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 30.2%;
Matches 26; Conservative
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Matches 31; Conservative
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A; Residues: 1-102 <MAN>
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Streptomyces wedmorensis

C; Date: 19-War-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999

C; Accession: S60207

C; Accession: S60207

R; Hidaka, T.; Goda, M.; Kuzuyama, T.; Takei, N.; Hidaka, M.; Seto, H.

Mol. Gen. Genet. 249, 274-280, 1995

A; Title: Cloning and nucleotide sequence of fosfomycin biosynthetic genes of Streptomyce

A; Reference number: S60207; MUID: 96091152

A; Accession: S60207

A; Status: nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-372 (HID)
A;Cross-references: EMBL:D38561; NID:g1060999; PIDN:BAA32488.1; PID:d1008145; PID:g10610
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
C;Genetics:
A;Gene: fonF
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A;Cross-references: EMBL:AL032684; PIDN:CAA21800.1; GSPDB:GN00067; SPDB:SPBP8B7.15c A;Experimental source: strain 972h-; clone pl p8B7 C;Genetics: A;Genetics: SPDB:SPBP8B7.15c A;Gene: SPDB:SPBP8B7.15c A;Gene: SPDB:SPBP8B7.15c A;Gene: SPDB:SPBP8B7.15c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Zea mays (maize)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 24-Oct-1997
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 24-Oct-1997
C;Accession: $61459
Biant Mol. Biol. 29, 841-856, 1995
A;Title: Expression of heat shock factor and heat shock protein 70 genes during maiz A;Reference number: $61448; MUID: 96128025
A;Reference number: $61448; MUID: 96128025
A;Recession: $61459
A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule: type: mRNA
A;Residues: 1-94 cGAG>
C;Genetics:
                                                                                                                                                                                                                                4;
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                                                                                                                                                                                                                                                                                                 237 IGPFDYPTADALVAASLLPARAAVAAGRFTGQDAAPAAPHAPLLSVDAVTLLYAVLGTH-R 295
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                                                                                                                                                                                                                                                                      10 DFPVKDAVEKFPAPLLYVCWENHLMFPAPFCLPLPPDMP---FGALAGDVL----PPVY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------EKFPAP-----LLYVCWENHLM 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 FPA--PFCLPLPPDMPFGALA-GDVLPPVYGYHPDFAKIDWDRVEWFRSGE----PWAPD 87
                                                                                                                                                                                                                             20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39; Indels
                                                                                                                                                                        Length 482;
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                                                                                                                                                                                                                           22; Indels
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                                                                                                                                                                             DB 2;
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Pred. No. 14;
8; Mismatches
                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                             Score 68;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fomF protein - Streptomyces wedmorensis
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26.2%;
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Best Local Similarity 33.3%;
Matches 23; Conservative
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Best Local Similarity
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| PA 353
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8

9

Gaps

37;

Length 102;

DB 2;

3.9;

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

September 26, 2000, 20:30:09; search time 58.11 Seconds (without alignments) 62.927 Million cell updates/sec Run on:

US-09-430-029-6 666 I MAVIALKPYDFPVKDAVEKF......HKDLISFRTPGLDGLGGASF 118 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

85661 seqs, 30989116 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_38:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Decorintion		P19733 pseudomonas	Q01551 burkholderi					Q23949 drosophila	090476 brachydanio	P97609 rattus norv	P17676 homo sapien									P02831 mus musculu	P25708 bos taurus	P00736 homo sapien	_	P44068 haemophilus		P51519 bovine leuk	_		Q39172 arabidopsis	Q04650 mesocricetu	O14641 homo sapien	•	256	Q03567 caenorhabdi
SUMMARIES	Ę		DMPO_PSESP	TBUD_BURPI	HAIR_HUMAN	TPS1_YEAST	FDHD_ALCEU	PPCM_HUMAN	TRSF_DROHY	LIM1_BRARE	HAIR_RAT	CEBB_HUMAN	PHSA_STRAT	NUBM_HUMAN	PRCC_HUMAN	DPS1_PINST	DPS2_PINST	MYCN_XENLA	VL2_HPV48	P2_ARATH	HXA3_MOUSE	NUBM_BOVIN	C1R_HUMAN	HAIR_MOUSE	Y882_HAEIN	CP4B_HUMAN	ENV_BLV	GAG_MLVDU	SRA4_RAT	P1_ARATH	LMX1_MESAU	DVL2_HUMAN	PHR_THETH	ASSY_METVA	YLD2_CAEEL
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	Query Match Length DR	6112	119	670	1189	495	286	640	201	405	1181	345	642	464	491	396	396	437	505	342	443	464	705	1182	245	511	515	529	1048	345	382	736	420	397	493
di	Query		32.4	19.1	11.1	10.9	10.7	10.7	10.2	10.1	10.1	10.0		8.	8.	9.7	9.7	7.6	9.7	9.6	9.6	9.6	9.6	9.6	9.5	9.2	9.5	9.5	9.5	٠			9.3	9.5	9.5
	Score		215.5	127	74	72.5	71.5	71.5	89	67.5	67	66.5	99	65	65	64.5	64.5	64.5	64.5	64	64	64	64	64	63.5	63.5	63	63	63	62.5	62.5	62.5	62	61.5	61.5
	Result		1	7	3	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

P73077 synechocyst P40453 saccharomyc 005017 oryctcolagus P34132 homo sapien P43562 saccharomyc 000482 homo sapien P36581 schizosacch P18111 mus musculu 005502 gallus gall 0600505 thermus aqu P30837 homo sapien	PERSE STANDARD; PRT; 119 AA. PEB-1991 (Rel. 17, Created) PEB-1991 (Rel. 17, Last sequence update) PEB-1991 (Rel. 17, Last sequence update) OL HYDROXILASE 4 PROTEIN (EC 1.14.13.7) (PHENOL 2-MONOOXYGENASE OMENOWENT) OR PHEA5; JOONEOURENT) R PROTEIN (EC 1.14.13.7) (PHENOL 2-MONOOXYGENASE JOONEOURENT) OR PHEA5; JOONEOURENT OR OF THE ACTION (ACTION OF THE ACTION OF THE ACTIVITY: PHENOL + NADPH + O(2) = CATECHOL + NADP(+) + R(2) OF THE ACTIVITY: PHENOL + NADPH + O(2) = CATECHOL + NADP(+) + R(2) OF THE ACTIVITY: PHENOL HYDROTHALDES THE ACTIVITY: PHENOL HYDROTHALDES TO STAND THE ACTIVITY: PHENOL HYDROTHALDES TO STAND OF THE ACTIVITY: PHENOL HYDROTHALDES TO STAND OF THE ACTIVITY: PHENOL HYDROTHALDES TO STAND OF THE ACTIVITY: PHENOL HYDROTHALDES TO STAND OF THE ACTIVITY: PHENOL HYDROTHALDES TO STAND OF THE ACTIVITY: THE MULTICHORORAL STAND OF THE ACTIVITY: THE MULTICHORORAL STAND OF THE ACTIVITY: THE MULTICHORORAL STAND OF THE ACTIVITY: THE MULTICHORORAL STAND OF THE ACTIVITY: THE MULTICHORORAL STAND OF THE ACTIVITY: THE MULTICHORORAL STAND OF THE ACTIVITY: THE MULTICHORORAL STAND OF THE ACTIVITY: THE MULTICHORORAL STAND OF THE ACTIVITY: THE MULTICHORORAL STAND OF THE ACTIVITY: THE MULTICHORORAL STAND OF THE ACTIVITY: THE MULTICHORORAL STAND OF THE ACTIVITY: THE MULTICHORORAL STAND OF THE ACTIVITY: THE MULTICHORORAL STAND OF THE ACTIVITY: THE MULTICHORORAL STAND OF THE ACTIVITY: THE MULTICHORORAL STAND OF THE ACTIVITY: THE MULTICHORORAL STAND OF THE ACTIVITY OF THE ACTIVITY OF THE ACTIVITY OF THE ACTIVITY OF THE ACTIVITY OF THE ACTIVITY OF THE ACTIVITY OF THE ACTIVITY OF THE ACTIVITY OF THE ACTIVITY OF THE ACTIVITY OF THE ACTIVITY OF THE ACTIVITY OF THE ACTIVITY OF THE ACTIVITY OF THE ACTIVIT	ism; Oxidoreductase; Monooxygenase; ; Plasmid. AE0151A918638C49 CRC64; Score 215.5; DB 1; Length 119; Pred. No. 2.5e-15; ; Mismatches 54; Indels 1; Gaps 1;
PARC_SYNY3 UBP7_YEAST PHLX_RABIT WY6A_HUMAN YFE0_YEAST NR52_HUMAN CALX_SCHPO CDX1_MOUSE HMPH_CHTCK PROB_THETH PROB_THETH DHAS_HUMAN	119 119 114.11 114.11 114.11 114.11 114.11 115.11 1	ol w; 18
9.2 920 9.2 1071 9.2 1458 9.2 257 9.2 540 9.2 560 9.1 268 9.1 376 9.1 376	PO_PSESP STANDARD; PRT; 9733; PEB-1991 (Rel. 17, Created) PEB-2000 (Rel. 39, Last sequence PEB-2000 (Rel. 39, Last sequence PEB-2000 (Rel. 39, Last annotation ENOL HYDROXYLASE P4 PROTEIN (EC 1 COMPONENT). PO OR PHEAS. Bamid pV1150. Cateria; Proteobacteria. DIENCE FROM N.A. DIENCE FROM N.A. DIENCE FROM N.A. Bacteriol. 172:6826-6833(1990). DIENCE FROM N.A. RAIN-BH; DERIVATIVES PHENOL, AN INTAME DIENCE FROM N.A. RAIN-BH; DERIVATIVES PHENOL, HAMA. IN VITRO PHENOL HYDROXYLASE FOR IN VITRO PHENOL HYDROXYLASE FOR IN VITRO PHENOL HYDROXYLASE FOR IN VITRO PHENOL HYDROXYLASE FOR PHENOL, AN DERIVATIVES. PA IS REQUIRED FOR IN VITRO PHENOL HYDROXYLASE FOR PHENOL HYDROXYL	37831. ocarbons otein; FR AA; 13
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	28. O	DR KW KW SQ Qu Qu Ma

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RESULT 3
HAIR_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- COFACTOR: FAD.
-!- PATHWAY: FIRST STEP OF PHENOL BIODEGRADATION.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE PHEA/TFDB FAMILY OF FAD MONOOXYGENASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAVIALKPYDFPVKDAVEKFPA-PLLYVCWENHLMFPAPFCLPLPPDMPFGALAGDVLPP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----LYVCWENHLMFPA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRIN-PRO1;
MEDLINE; 93015703.

MEDLINE; 93015703.

"Complete nuclectide sequence of tbuD, the gene encoding phenol/cresol hydroxylase from Pseudomonas pickettii PKO1, and functional analysis of the encoded enzyme.";

J. Bacteriol. 174:6518-6526(1992).

-I - CATALYTIC ACTIVITY: PHENOL + NADPH + O(2) = CATECHOL + NADP(+) + H(2)O (ACTS ALSO ON MONOHYDROXY-, MONOHALO-, MONOAMINO- AND MONOMETHYLDHENOLS).
                        60 VYGYHPDFAKIDWDRVEWFRSGEPWAPDPAKSLAGNGLGHKDLISFRTPGLDGLGGA 116
                                                                                                            38 PFCLPLPPDMPFGALAGDVLPPVYGYHPDFAK----IDWDRVEWFRSGEPWAPDPAKS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM: PF01360; Monooxygenase; 1.
Aromatic hydrocarbons catabolism; Oxidoreductase; Monooxygenase; Ravoprotein; FAD; NADP.
INIT.MET 0 0 | FAD (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; beta subdivision; Raistonia group;
Raistonia.
                                                                                                                                                                                                                                                                               01-JUL-1993 (Rel. 26, Created)
1-JUL-1993 (Rel. 26, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PHENOL 2-MONOOXYGENASE (EC 1.14.13.7) (PHENOL HYDROXYLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Score 127; DB 1; Length 670; | Pred. No. 1.6e-05; | Mismatches 28; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D (POTENTIAL).
90A925D94C19C837 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       Burkholderia pickettii (Pseudomonas pickettii).
                                                                                                                                                                                                                                        670 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 1-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAVIA-LK--PYDFPVKDAVEKFPAPL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 ----LAGNGLGHKDLISFRTPGLDGLG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296 EGRVFLAGDA-----RHRHPPLTGIG 316
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670 AA; 72867 MW
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ilarity 27.78; |
Conservative 13
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                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A45730.
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es 41; Conserv
                                                                                                                                                                                                                                                          Q01551;
01-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A45730
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SEQUENCE
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Matches
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- I - FUNCTION: MAY ACT AS A TRANSCRIPTION FACTOR THAT.COULD ACT ON TO REGULATE ONE OF THE PHASES OF HAIR GROWTH.

C - SUBCELLULAR LOCATION: NUCLEAR.

- I - ALTERNATIVE PRODUCTS: AT LEAST TWO FORMS ARE PRODUCED BY ALTERNATIVE SPLICING.

C - I - SISEASE: DEFECTS IN HR ARE THE CAUSE OF ALOPECIA UNIVERSALIS

C - I - DISEASE: DEFECTS IN HR ARE THE CAUSE OF HAIR LOSS. IT IS

C - ALTERNATIZED BY HAIR FOLLICLES WITHOUT HAIR.

C - I - DISEASE: DEFECTS IN HR ARE THE CAUSE OF AIRPICHIA WITH PAPULAR

C - I - DISEASE: DEFECTS IN HR ARE THE CAUSE OF AIRCHIA WITH PAPULAR

C - I - DISEASE: DEFECTS IN HR ARE THE CAUSE OF AIRCHIA WITH PAPULAR

C - I - DISEASE: DEFECTS IN HR ARE THE CAUSE OF AIRCHIA WITH PAPULAR

C - I - DISEASE: DEFECTS IN HR ARE THE CAUSE OF HAIR.

C - I - DISEASE: DEFECTS IN HR ARE THE CAUSE OF HAIR.

C - I - DISEASE: DEFECTS IN HR ARE THE CAUSE OF HAIR.

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C - I - DISEASE: DEFECTS IN HR ARE THE CAUSE OF HAIR.

C - I - DISEASE: DEFECTS IN HR ARE THE CAUSE OF HAIR.

C - I - DISEASE OF THE BODY AND ALMOST COMPLETE ABSENCE OF HAIR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ahmad W., Ul Haque M.F., Brancolini V., Tsou H.C., Ul Haque S.,
Lam H., Aita V.M., Owen J., Deblaquiere M., Frank J.,
Cserhalmi-Friedman P.B., Leask A., McGrath J.A., Peacocke M.,
Ahmad M., Ott J., Christiano A.M.;
"Alopecia universalis associated with a mutation in the human hairless
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 98409496.
Citchon S., Anker M., Vogt I.R., Rohleder H., Putzstuck M., Hillmer A., Farcog S.A., Al-Dhafri K.S., Ahmad M., Haque S., Rietschel M., Propping P., Kruse R., Nothen M.M.; "Clohing, genomic organization, alternative transcripts and mutational analysis of the gene responsible for autosomal recessive universal congenital alopecia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ahmad W., Irvine A.D., Lam H., Buckley C., Bingham E.A.,
Panteleyev A.A., Ahmad M., McGrath J.A., Christiano A.M.;
"A missense mutation in the zinc-finger domain of the human hairless
gene underlies congenital atrichia in a family of Irish travellers.";
Am. J. Hum. Genet. 63:984-991(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zinc-finger; DNA-binding; Nuclear protein; Transcription regulation; Metal-binding; Alternative splicing; Disease mutation. ZN_FING 600 625 CG-TYPE. CA_TYPE. 620 620 620 R ^{-5} Q (IN APL).
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND VARIANT ALUNC ALA-1022
                                                                                                            15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
115-JULSS PROTEIN.
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/FTId=VAR_005265.
          1189 AA.
                PRT;
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                STANDARD;
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MIM; 209500; -.
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HAIR_HUMAN
O43593;
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